SUBJECT INDEX

A

ABC transporters
  capsular polysaccharide production and, 298, 308
Acanthurus nigrofuscus
  bacterial cell size and, 343
Acetate
  cobalamin synthesis and use, 152
Acetobacter spp.
  microalgal metabolites and, 435
Acetobacterium woodii
  F_0F_1-ATPases and, 792, 811
Acetyl-CoA
  cobalamin synthesis and use, 146–47
Acetylcholine
  coxsackieviruses and, 15
Acholeplasma laidlawii
  mycoplasmal molecular biology and, 28–30, 37–45
Acholeplasma oculi
  mycoplasmal molecular biology and, 38, 45
Acholeplasma spp.
  mycoplasmal molecular biology and, 36, 39, 41–42
Acid fast stain
  limitations of, 352
Acinetobacter calcoaceticus
  capsular polysaccharide production and, 287
  β-ketoadipate pathway and, 553
Acinetobacter eutrophus
  β-ketoadipate pathway and, 573
Acinetobacter spp.
  β-ketoadipate pathway and, 558–59, 574, 576
Acquired immunodeficiency syndrome (AIDS)
  evolutionary genetics and, 418
Actin
  M. grisea and, 491
Actinobacillus actinomycetemcomitans
  oral bacteria adhesion mechanisms and, 542
Actinobacillus pleuropneumoniae
  capsular polysaccharide production and, 299
Actinomadura spp.
  halogenated metabolites and, 380
Actinomyces spp.
  halogenated metabolites and, 383
  nucleic acid amplification and, 362
  oral bacteria adhesion mechanisms and, 533–37
Actinoplanus spp.
  halogenated metabolites and, 383
Actinosporangium vitaminophilum
  halogenated metabolites and, 378
Active immunization
  live attenuated varicella vaccine and, 78–79
Acyl coenzyme A
  genetically engineered synthesis and, 470
Adenosine triphosphate (ATP)
  capsular polysaccharide production and, 298
  cobalamin synthesis and use, 142–43
  F_0F_1-ATPases and, 810–14
Adenosyl transferases
  cobalamin synthesis and use, 170–71
Adhesins
  oral bacteria adhesion mechanisms and, 523–30
Adhesion mechanisms
  capsular polysaccharide production and, 287–88
  mycoplasmas and, 45–46
  oral bacteria and, 513–43
Adhesive disc
  G. lamblia and, 680, 682, 684–87
Ado-B_{12}
  synthesis and use, 138–73
Adrenal steroids
  tuberculosis pathogenesis and, 259, 270–71, 276–78
Aerobacter aerogenes
  capsular polysaccharide production and, 304
Aerobic respiration
  cobalamin synthesis and use, 138
Aeromonas hydrophila
  LuxR-LuxI type regulation and, 733
Afipia felis
  cat-scratch disease and, 714, 716–18, 720
Afipia spp.
  cat-scratch disease and, 707
Agrobacterium spp.
  β-ketoadipate pathway and, 575–76
Agrobacterium tumefaciens
  cobalamin synthesis and use, 150
  β-ketoadipate pathway and, 553, 558, 575, 577, 580–81
  rhizobacterial osmoadaptation and, 120, 125–56
Agrobacterium spp.
  rhizobacterial osmoadaptation and, 102, 119
Agrobacterium tumefaciens
  LuxR-LuxI type regulation and, 728, 730, 732, 735–36, 740–42, 746
Agronomy
  evolutionary genetics and, 402
ainS gene
  LuxR-LuxI type regulation and, 739, 744–45
ALB1 gene
  M. grisea and, 501–2
Alcaligenes eutrophus
  heavy metal resistances and, 780
  β-ketoadipate pathway and, 565
Alcaligenes spp.
  heavy metal resistances and, 756, 761–62, 780
  β-ketoadipate pathway and, 558, 574, 576
Alcohol
  enteroviruses and, 9
Aldolases
  genetically engineered synthesis and, 472–75
Aldols
  genetically engineered synthesis and, 472–74
Alexandrium catenella.
  microalgal metabolites and, 435
Alexandrium spp.
  microalgal metabolites and, 435, 440, 442, 455–56
Alexandrium tamarense
  microalgal metabolites and, 435, 447, 455–57
Alleles
  evolutionary genetics and, 408, 423

Allelic frequency
evolutionary genetics and, 423, 426
Aluminum salts
rhizobacterial osmoadaptation and, 106
Aminopropanol
cobalamin synthesis and use, 140, 156
Aminopropanol side chain
cobalamin synthesis and use, 156
Amphidinium carterae
microalgal metabolites and, 457
Amphidinium klebsii
microalgal metabolites and, 457
Amphidinium spp.
microalgal metabolites and, 435, 439–41, 444–45, 453, 457
Amphiscolops spp.
microalgal metabolites and, 439
Amycolatopsis orientalis
halogenated metabolites and, 379
Amylases
polysaccharide hydrolysis and, 183
Anabaena circiralis
microalgal metabolites and, 436, 455
Anaerobic fermentation
cobalamin synthesis and use, 138, 142
Anaeroplasma spp.
mycoplasmal molecular biology and, 28–29
Antibiotics
cat-scratch disease and, 711
enteroviruses and, 9
spontaneous mutators and, 639
Antibodies
cat-scratch disease and, 716, 718
enteroviruses and, 10, 14
G. lamblia and, 686, 694
live attenuated varicella vaccine and, 75
poliovirus and, 4–6
tuberculosis pathogenesis and, 265
Antigens
capsular polysaccharide production and, 286–87, 289–92, 302–4
cat-scratch disease and, 718, 721
G. lamblia and, 681–82, 700
limitations of detection, 352
mycoplasmas and, 46–48
tuberculosis pathogenesis and, 272–73, 279
Antimony
heavy metal resistances and, 755, 766–68
Aphanizomenon flos-aquae
microalgal metabolites and, 436, 447, 449, 455, 457
Aplysia spp.
microalgal metabolites and, 459
Apomorphy
evolutionary genetics and, 423
Appressorium
M. grisea and, 491, 495–99, 503–6
Arabidopsis thaliana
heavy metal resistances and, 776
Archaea
bacterial cell size and, 317
cobalamin synthesis and use, 140, 142, 147
F_0F_1-ATPases and, 793
β-ketoadipate pathway and, 558
Archaebacteria
halogenated metabolites and, 383
Aromatic ring cleavage
β-ketoadipate pathway and, 555
Arsenate reductase
heavy metal resistances and, 769–70
Arsenic
heavy metal resistances and, 754–55, 766–68
Arsenite efflux ATPase
heavy metal resistances and, 768–69
Arthrobacter spp.
β-ketoadipate pathway and, 556, 559, 563
Aspergillus nidulans
evolutionary genetics and, 416
Aspergillus oryzae
polysaccharide hydrolysis and, 193
Aspergillus spp.
β-ketoadipate pathway and, 558
Asteroleplasma anaerobium
mycoplasmal molecular biology and, 28–29
Asteroleplasma spp.
mycoplasmal molecular biology and, 28
ATPases
heavy metal resistances and, 754
atp operon
F_0F_1-ATPases and, 793–94
Autoimmune disease
nucleic acid amplification and, 352
Autoinducers
LuxR-LuxI type regulation and, 727, 729, 731, 735–40
Vibrio fischeri-Euprymna scolopes symbiosis and, 616–17
Auxotrophy
amino acid
Vibrio fischeri-Euprymna scolopes symbiosis and, 616
Axonemes
G. lamblia and, 686
Azomonas spp.
β-ketoadipate pathway and, 558
Azospirillum brasilense
rhizobacterial osmoadaptation and, 103, 111–13, 115, 118, 121–22, 126
Azospirillum halopraeferens
rhizobacterial osmoadaptation and, 118, 126
Azospirillum lipoferum
rhizobacterial osmoadaptation and, 115
Azospirillum spp.
β-ketoadipate pathway and, 558, 568
rhizobacterial osmoadaptation and, 101–3, 108, 111–12, 115–16, 118–19, 126
Azotobacter spp.
β-ketoadipate pathway and, 558, 573, 576
rhizobacterial osmoadaptation and, 102
Azotobacter vinelandii
β-ketoadipate pathway and, 562

B

Babesia microti
nucleic acid amplification and, 357
Babesia spp.
nucleic acid amplification and, 357
Bacillariophyta
microalgal metabolites and, 434
Bacillary angiomatosis
cat-scratch disease and, 714–15, 718
Bacille Calmette Guérin
tuberculosis pathogenesis and, 259, 263–64, 266, 272–73
Bacillus brevis

rhizobacterial osmoadaptation and, 103
Bacillus caldotenax
F_0F_1-ATPases and, 810
Bacillus circulans
polysaccharide hydrolysis and, 190, 192–94
rhizobacterial osmoadaptation and, 103
Bacillus megaterium
cobalamin synthesis and use, 148
rhizobacterial osmoadaptation and, 103
Bacillus polymyxa
rhizobacterial osmoadaptation and, 103
Bacillus spp.
bacterial cell size and, 320, 329
F_0F_1-ATPases and, 806–7
heavy metal resistances and, 755, 757, 768, 773, 775, 777–78, 782
β-ketoadipate pathway and, 556
microalgal metabolites and, 435
Bacillus stearothermophilus
F_0F_1-ATPases and, 810
polysaccharide hydrolysis and, 193
Bacillus subtilis
evolutionary genetics and, 419
heavy metal resistances and, 755
LuxR-LuxI type regulation and, 745
mycoplasmal molecular biology and, 33, 36–37, 44
Bacterial-animal association
cooperative, 591–618
Bacterial cell size
biological constraints, 319–20
catastrophe kit and lower limit on cell size, 325–27
diversity, size, and shape, 344
effect of shape, 342
evolution, 320–23
factors controlling, 321
factors determining how big a single cell could be
metabolism, 341
shell nature of centrally vacuolated cell, 341–42
temperature, 341
time, 341
fish gut bacteria, 342–44
formulation of steady-state diffusion for growing cell
consumption and generation of substances, 337
consumption in cytoplasm, 334–39
diffusion and convection, 336
diffusion through structured environment, 337–38
diffusion with binding, 337
diffusion within cytoplasm, 338–39
diffusion with reaction, 337
through environment and cell surface, 334–39
unstirred layer, 337
lower size extreme, 318, 341
nutritional deprivation and environmental adversity, 327–28
physiological changes lead to immunity from environmental conditions, 327–34
prokaryote size and process of wall enlargement, 323–25
quiescent cells in low-dilution rate chemostats, 329–30
'shut down' cell, 328–29
small bacterial cells, 340–41
surface-to-volume question, 339–40
switch to starvation conditions, 333–34
upper size extreme, 319, 342–44
viable-but-not-culturable bacteria, 331–33
Bacterial communication
oral bacteria adhesion mechanisms and, 542–43
Bacterial probes
Vibrio fischeri-Euprymna scolopes symbiosis and, 618
Bacteria-plant interactions
capsular polysaccharide production and, 290
Bacteriophage Mu
bacterial cell size and, 325
Bacteriophage T4
bacterial cell size and, 338
Bacteroides ovatus
polysaccharide hydrolysis and, 196
Bacteroids
rhizobacterial osmoadaptation and, 123–24
Bartonella bacilliformis
cat-scratch disease and, 718–20
Bartonellaceae
cat-scratch disease and, 719
Bartonella doshiae
cat-scratch disease and, 719
Bartonella elizabethae
cat-scratch disease and, 719
Bartonella grahamii
cat-scratch disease and, 719
Bartonella hensenale
cat-scratch disease and, 707, 719–21
nucleic acid amplification and, 351
Bartonella peromysci
cat-scratch disease and, 719
Bartonella quintana
cat-scratch disease and, 719–20
Bartonella spp.
cat-scratch disease and, 718–21
Bartonella talpae
cat-scratch disease and, 719
Bartonella taylorii
cat-scratch disease and, 719
Bartonella vinsonii
cat-scratch disease and, 719
Basal bodies
G. lamblia and, 686
Baseball glove model
heavy metal resistances and, 773
Beggiatoa spp.
bacterial cell size and, 342
Beijerinckia spp.
β-ketoadipate pathway and, 558
ben genes
β-ketoadipate pathway and, 575, 577
Benzoate
β-ketoadipate pathway and, 564
Berkeley bodies
G. lamblia and, 684
bet genes
rhizobacterial osmoadaptation and, 109
bex genes
capsular polysaccharide production and, 296–97, 300
Binary encapsulation
capsular polysaccharide production and, 308
Binding
bacterial cell size and, 337
Biological diversity
evolutionary genetics and, 413, 415, 422
Biological fossils
G. lamblia and, 682, 702
Bioluminescence
V. fischeri and, 596–97
Biotechnology
halogenating enzymes and, 393–94
Blackman model
bacterial cell size and, 332
Blastomyces dermatitides

nucleic acid amplification and, 356
Borrelia burgdorferi
nucleic acid amplification and, 357–59
Botulinum toxin
coxsackieviruses and, 15
Br^-
halogenated metabolites and, 375
Bradyrhizobium japonicum
β-ketoadipate pathway and, 568–69
rhizobacterial osmoadaptation and, 114, 116, 120, 123, 128
Bradyrhizobium spp.
β-ketoadipate pathway and, 558, 575
rhizobacterial osmoadaptation and, 116, 119, 121
Brain-to-brain passage
poliovirus and, 4
Branch convergence
β-ketoadipate pathway and, 553, 573–74
Branched DNA (bDNA) assay
nucleic acid amplification and, 353
Brevibacterium fuscum
β-ketoadipate pathway and, 562
Bryopsis spp.
microalgal metabolites and, 443
btu genes
cobalamin synthesis and use, 154, 159–62, 164–67
BUF1 gene
M. grisea and, 501, 502
Buffalo green monkey (BGM) cells
enteroviruses and, 14
Burkholderia cepacia
β-ketoadipate pathway and, 562, 575
Burkholderia spp.
β-ketoadipate pathway and, 558
Butyrivibrio fibrosolvens
polysaccharide hydrolysis and, 196

C

C3b
capsular polysaccharide production and, 288–89
CadA Cd^{2+} ATPase
heavy metal resistances and, 757–58
Cadmium
heavy metal resistances and, 755–58
Caenorhabditis elegans
evolutionary genetics and, 404
Cairnsian mutations
bacterial cell size and, 326
Calcitriol
tuberculosis pathogenesis and, 275–77
Caldariomyces fumago
halogenated metabolites and, 388–89
Caldocellulosiruptor saccharolyticus
polysaccharide hydrolysis and, 199
Caldocellum saccharolyticum
polysaccharide hydrolysis and, 199
Caltractin
G. lamblia and, 686
Canada
live attenuated varicella vaccine and, 79–85
Cancer susceptibilities
spontaneous mutators and, 625, 638–39
Candida albicans
evolutionary genetics and, 414, 416
cap gene cluster
capsular polysaccharide production and, 297, 300
Capnocytophaga spp.
oral bacteria adhesion mechanisms and, 540
Capsular polysaccharide
biochemistry of capsule production in gram-negative bacteria, 297
export of group II polysaccharides, 298–302
group I polysaccharide biosynthesis, 304
group II polysaccharide biosynthesis, 302–4
capsule diversity generation, 306–8
functions of bacterial capsules
adherence, 287–88
bacteria-plant interactions, 290
prevention of dessication, 287–88
resistance to nonspecific host immunity, 287–89
resistance to specific host immunity, 287, 289
genetics of capsule gene clusters in gram-negative bacteria
capsule gene cluster analysis from other gram-negative bacteria, 296–97
capsule gene clusters in *E. coli*, 290–91
group I K antigens, 291–92
group II K antigens, 292–96
group III K antigens, 296
genetics of capsule production in gram-positive bacteria, 304–6
introduction, 286–87
perspectives, 308
rhizobacterial osmoadaptation and, 129
Carbohydrate synthesis
genetically engineered synthesis and, 467, 472–77
Carbon
Vibrio fischeri-Euprymna scolopes symbiosis and, 603
Carbon dioxide
bacterial cell size and, 344
Carboxysome protein homologues
cobalamin synthesis and use, 170
Catabolism
genetically engineered synthesis and, 472–77
pectinolysis regulation in *E. chrysanthemi* and, 222–25, 229
Catalysis
bacterial cell size and, 317
Catastrophe kit
bacterial cell size and, 317, 325–27
Catechol
β-ketoadipate pathway and, 553, 560, 564
cat genes
β-ketoadipate pathway and, 561–75, 577, 579–80
Cation resistance systems
heavy metal resistances and, 781
Cat-scratch disease
clinical perspectives and pathology, 710–11
expanding spectrum of disease associated with *Bartonella*, 719
future research, 720–21
hindsight observations, 719–20
historical epidemiology, 709–10
historical perspective, 708–9
nomenclature change to *Bartonella* from

Rochalimaea, 718–19
search for agent, 712–18
Caulobacter crescentus
bacterial cell size and, 324–25, 328, 331, 342
chi genes
cobalamin synthesis and use, 152, 156–57
CD1
tuberculosis pathogenesis and, 263–64
CDP-D-abequose
genetically engineered synthesis and, 474, 476
Cell culture
limitations of, 352
Cell density dependence
LuxR-LuxI type regulation and, 727–28, 731
Cell differentiation
G. lamblia and, 682
Cell-free reactions
genetically engineered synthesis and, 467
Cell-mediated immunity
live attenuated varicella vaccine and, 74–75
Cell size
bacterial, 317–44
Cell surface
bacterial cell size and, 334–39
Cellular protruberance
M. grisea and, 491
Cellulomonas fimi
polysaccharide hydrolysis and, 190, 199–201
Cellulomonas uda
polysaccharide hydrolysis and, 200
Central nervous system (CNS)
coxsackieviruses and, 15–16
nucleic acid amplification and, 359
poliovirus and, 5–6
Centrally vacuolated cell
bacterial cell size and, 341–42
Centrin
G. lamblia and, 686
Centrocetos clavulatum
microalgal metabolites and, 445
Cerebrospinal fluid (CSF)
enteroviruses and, 17
Cervicitis
nucleic acid amplification and, 360
CF tests
enteroviruses and, 12
Chagas' disease
evolutionary genetics and, 403, 409, 412–15
Chaina rubra
halogenated metabolites and, 379
Chaperonins
LuxR-LuxI type regulation and, 746
Chemiosmotic antiporter
heavy metal resistances and, 761–62
Chemostats
low-dilution
bacterial cell size and, 329–30
Chemotaxis
β-ketoadipate pathway and, 568–72
Chemotherapy
enteroviruses and, 9
tuberculosis pathogenesis and, 261, 275
Chemotrophic metabolism
bacterial cell size and, 342
Chickenpox
live attenuated varicella vaccine and, 60
Children
G. lamblia and, 681
live attenuated varicella vaccine and, 60–90
Chitin
polysaccharide hydrolysis and, 184, 193–95
Chitinases
polysaccharide hydrolysis and, 183
Chlamydia pneumoniae
nucleic acid amplification and, 356
Chlamydia trachomatis
nucleic acid amplification and, 351–52, 360
Chloramphenicol
halogenated metabolites and, 386–87
Chlorine
enteroviruses and, 9
Chlorocatechol
β-ketoadipate pathway and, 553
Chloroform
enteroviruses and, 11
Chlorophyll
cobalamin synthesis and use, 138, 140
Chlorophyta
microalgal metabolites and, 434
7-Chlorotetracycline
halogenated metabolites and, 384–85
Choline
rhizobacterial osmoadaptation and, 110–11, 117–18
Chondria armata
microalgal metabolites and, 443
Chromate
heavy metal resistances and, 780–81
Chromosomes
heavy metal resistances and, 756
mycoplasmas and, 35–37
Chrysophaeum taylori
microalgal metabolites and, 446, 448
Chrysophyta
microalgal metabolites and, 434
chv genes
rhizobacterial osmoadaptation and, 121
Ciliphora
microalgal metabolites and, 434
cis-acting promoter elements
LuxR-LuxI type regulation and, 740–41
rRNA transcription in *E. coli* and, 649–63
Cistrons
pectinolysis regulation in *E. chrysanthemi* and, 214
Citrobacter freundii
cobalamin synthesis and use, 172
Cl^-
halogenated metabolites and, 375
rhizobacterial osmoadaptation and, 104
Cladistics
evolutionary genetics and, 410, 423, 426
Clonality
evolutionary genetics and, 401, 405–8, 410, 412–16, 418–19, 421–24
mycoplasmas and, 44–45
Clonet
evolutionary genetics and, 420, 424
Clostridium acetobutylicum
β-ketoadipate pathway and, 565
Clostridium cellulolyticum
polysaccharide hydrolysis and, 199
Clostridium cellulovorans
polysaccharide hydrolysis and, 198
Clostridium stercorarium
polysaccharide hydrolysis and, 199
Clostridium thermocellum

polysaccharide hydrolysis and, 192, 197–99
Clostridium spp.
polysaccharide hydrolysis and, 192, 197
CMS structures
Vibrio fischeri-Euprymna scolopes symbiosis and, 605, 607
Coaggregation partnerships
oral bacteria adhesion mechanisms and, 517–19
Cobalamin (coenzyme B_{12})
B_{12}-dependent reactions, 143–44
acetyl-CoA synthesis, 146
in enteric bacteria, 144–46
epoxyqueosine reductase, 146
ethanolamine ammonia lyase, 144–46
glycerol dehydratase, 146
methionine synthetase, 146
methyl transfer in methane-producing Archaea, 147
propanediol dehydratase, 144
ribonucleotide reductases, 147
biosynthesis
Ado-B_{12} completion, 159
aminopropanol side chain source, 156
cobalt reduction, 156
corrin ring, 151–53
deoxyadenosyl moiety addition, 154–56
dimethylbenzimidazole nucleoside formation, 158–59
dimethylbenzimidazole synthesis, 156–58
first enzyme in B_{12} synthesis, 153
enteric bacteria
B_{12} adenosyl transferases, 170–71
B_{12} paradox, 166–67, 171
carboxysome protein homologues, 170
ethanolamine metabolism, 168
pdu and *eut* operon genetic analysis, 168–69
propanediol metabolism, 167–68
regulation of B_{12}-dependent functions, 169 *Salmonella* growth in host organism, 171–72
general aspects of B_{12} synthesis
comparison of genes from *Salmonella* and *Pseudomonas* spp., 151
genetic analysis of B_{12} synthesis in *P. denitrificans*, 150–51
genetic analysis of B_{12} synthesis in *S. typhimurium*, 148–50
genetically engineered synthesis and, 467, 482–87
introduction, 138–39
ancient origins, 141–42
distribution among living forms, 141, 143
structure, 139–40
regulation of B_{12} synthesis in *S. typhimurium*
cob operon and *btuB* gene control by Ado-B_{12}, 164–67
cob/pdu regulon control, 162–64
transport
across inner membrane, 161–62
across outer membrane, 159–61
Cobalt insertion
cobalamin synthesis and use, 138, 151, 153–54, 156
Cobinamide
cobalamin synthesis and use, 140
cob operon
cobalamin synthesis and use, 149–54, 156–59, 164–67
cob/pdu regulon
cobalamin synthesis and use, 162–64
Cobyric acid
cobalamin synthesis and use, 140, 156
Cobyrinic acid
cobalamin synthesis and use, 152
Coccidioides immitis
nucleic acid amplification and, 356
Cocksackieviruses
discovery and classification of, 1, 3, 6–12, 15–16, 18–19
Co-evolution
evolutionary genetics and, 404
Cofactor regeneration
genetically engineered synthesis and, 469–71
Colonization
Vibrio fischeri-Euprymna scolopes symbiosis and, 591, 597–609
Comamonas acidovorans
β-ketoadipate pathway and, 573, 576
Comamonas spp.
β-ketoadipate pathway and, 558, 573, 575
Comamonas testasteroni
β-ketoadipate pathway and, 576
Compartmentalization
evolutionary genetics and, 402–3
Compatible solute synthesis
rhizobacterial osmoadaptation and, 112–14
Complement fixation antigens
enteroviruses and, 12
Conidia
M. grisea and, 493–95
Conjugal transfer
TN*916* and, 42–43
Conjugation
Vibrio fischeri-Euprymna scolopes symbiosis and, 610
Convection
bacterial cell size and, 336
CopA ATPase
heavy metal resistances and, 762–64
CopB ATPase
heavy metal resistances and, 762–64
Copiotrophs
bacterial cell size and, 333
Copper
heavy metal resistances and, 755–65
Core promoters
rRNA transcription in *E. coli* and, 649–51
Corrinoids
cobalamin synthesis and use, 138–39, 147, 154
Corrins
cobalamin synthesis and use, 151–53
genetically engineered synthesis and, 482–87
Cortisol
tuberculosis pathogenesis and, 276–78
Cortisone
tuberculosis pathogenesis and, 276, 278
Corynebacterium

hydrocarboclastus
halogenated metabolites and, 387
Cost-benefit studies
live attenuated varicella vaccine and, 89
Coxiella spp.
nucleic acid amplification and, 352
cpoF gene
halogenated metabolites and, 392
cps gene cluster
capsular polysaccharide production and, 292, 297, 299, 305–6
p-Cresol
β-ketoadipate pathway and, 553
Cross-fertilization
evolutionary genetics and, 416
CRP protein
pectinolysis regulation in *E. chrysanthemi* and, 214
Crypt
light organ, 612–17
Cryptic speciation
evolutionary genetics and, 418–19, 422
Cryptococcus neoformans
evolutionary genetics and, 416
nucleic acid amplification and, 359
Cryptophyta
microalgal metabolites and, 434, 445
ctr genes
capsular polysaccharide production and, 297, 300
cut genes
heavy metal resistances and, 765–66
Cyanobacteria
heavy metal resistances and, 754, 756, 778–80
Cyclic adenosine monophosphate (cAMP)
Vibrio fischeri-Euprymna scolopes symbiosis and, 616
Cycling probe technology
nucleic acid amplification and, 353
Cyclosporin A
tuberculosis pathogenesis and, 276
Cylindrospermopsis raciborskii
microalgal metabolites and, 449
cysG gene
cobalamin synthesis and use, 141, 150, 153
Cysteine-rich proteins
G. lamblia and, 679, 694–95
Cysteine thiolates
heavy metal resistances and, 754
Cysts
G. lamblia and, 679–80, 682, 684, 688, 690–700
Cytokines
tuberculosis pathogenesis and, 259, 264–65, 267–77
Cytoplasm
bacterial cell size and, 334–39
G. lamblia and, 687
Cytoskeleton
G. lamblia and, 685–87

D

dam gene
spontaneous mutators and, 635
Data weighting
evolutionary genetics and, 419–20
Dehalogenation
halogenated metabolites and, 393
Dehydroepiandrosterone (DHEA)
tuberculosis pathogenesis and, 276–78
Delayed-type hypersensitivity response
tuberculosis pathogenesis and, 268–70, 274
Dendrograms
evolutionary genetics and, 409–10, 426
Deoxyadenosyl moiety
cobalamin synthesis and use, 154–56
Deoxycholate
enteroviruses and, 9, 11
Deoxyuronate isomerase
pectinolysis regulation in *E. chrysanthemi* and, 223–24
Dessication
capsular polysaccharide production and, 287–88
Detergents
enteroviruses and, 9
Developed countries
tuberculosis pathogenesis and, 260
Development
Vibrio fischeri-Euprymna scolopes symbiosis and, 591
Diffusion
bacterial cell size and, 317, 334–39, 341, 343
Digenea simplex
microalgal metabolites and, 445
Dimethylbenzimidazole
cobalamin synthesis and use, 140, 156–59
Dinophysis spp.
microalgal metabolites and, 437, 458
Diploidy
evolutionary genetics and, 408, 424
Diplomonadida
G. lamblia and, 683
Directly-observed therapy
tuberculosis pathogenesis and, 261
Disc proteins
G. lamblia and, 685
Disinfectants
enteroviruses and, 9
DNA curvature
E. coli and, 656
DNA ligase
spontaneous mutators and, 629
DNA polymerases
spontaneous mutators and, 628, 631–32, 637–38
DNA repair
mycoplasmas and, 37
spontaneous mutators and, 625–26, 628–31 *dnaQ* gene
spontaneous mutators and, 628
DNA replication
mycoplasmas and, 35–37
Dollabella spp.
microalgal metabolites and, 459
Domains
polysaccharide hydrolysis and, 183–84, 190–92
Downstream studies
evolutionary genetics and, 404–5
Drosophila melanogaster
evolutionary genetics and, 404
Drosophila subatrata
halogenated metabolites and, 377
Drug resistance
evolutionary genetics and, 401, 404–5, 407, 415
nucleic acid amplification and, 362
spontaneous mutators and, 639

tuberculosis pathogenesis and, 260–61, 275
Du Toit stocks
enterovirus, 10
Dwarves
bacterial cell size and, 340
Dynein ATPase
G. lamblia and, 685

E

Echoviruses
discovery and classification of, 1, 6, 8–10, 13
Ecosystems
bacterial
census and consensus in, 727–46
Ectoine
rhizobacterial osmoadaptation and, 108, 110–11, 114, 116–17
Efflux systems
heavy metal resistances and, 754, 756, 768–69
Ehrlichia spp.
nucleic acid amplification and, 357
Eicosanoids
cyclic
microalgal metabolites and, 441–42
Einstein diffusion equation
bacterial cell size and, 338
Elderly
live attenuated varicella vaccine and, 60, 64
Electrical double layer
rhizobacterial osmoadaptation and, 105–6
Electron acceptors
cobalamin synthesis and use, 138, 140–42, 144, 146
Electron microscopy
enteroviruses and, 12
Electrophoretic type
evolutionary genetics and, 419, 424, 426
Electroporation
Vibrio fischeri-Euprymna scolopes symbiosis and, 610
Empirism
evolutionary genetics and, 403
EMS mutagenesis
spontaneous mutators and, 632
Encephalitis
nucleic acid amplification and, 359
Encystation-specific secretory vesicles
G. lamblia and, 679, 692–94
Endomembranes
G. lamblia and, 679, 681–84, 687–89
Endoplasmic reticulum (ER)
G. lamblia and, 679–80, 683–84
Energy transduction
bacterial cell size and, 342
Entamoeba histolytica
evolutionary genetics and, 414
G. lamblia and, 683
Entamoeba spp.
G. lamblia and, 683
Enteric bacteria
cobalamin synthesis and use, 138, 144–46, 153, 166–72
rhizobacterial osmoadaptation and, 108–10
Enteric infections
poliovirus and, 3
Enterobacter agglomerans
LuxR-LuxI type regulation and, 733
Enterobacter spp.
β-ketoadipate pathway and, 558
Enterococcus faecalis
LuxR-LuxI type regulation and, 728, 745
mycoplasmal molecular biology and, 42
Enterococcus hirae
bacterial cell size and, 328
F_0F_1-ATPases and, 793
heavy metal resistances and, 762–64
Enteroviruses
discovery and classification of, 1–20
Entomoplasma ellychniae
mycoplasmal molecular biology and, 29
Entomoplasma spp.
mycoplasmal molecular biology and, 28
Envelopes
bacterial cell size and, 330
LuxR-LuxI type regulation and, 727
Environmental conditions
bacterial cell size and, 317, 327–39
G. lamblia and, 681
heavy metal resistances and, 778
tuberculosis pathogenesis and, 273, 279
Enzyme immunoassay (EIA)
nucleic acid amplification and, 356
Enzyme-linked immunosorbent assay (ALISA)
enteroviruses and, 12
Enzymes
bacterial cell size and, 317, 330
genetically engineered synthesis and, 467, 479–82
halogenated metabolites and, 388–91, 393–94
β-ketoadipate pathway and, 557, 559, 561–66, 568, 574
M. grisea and, 506–7
polysaccharide hydrolysis and, 184, 187–90
Epidemic clonality
evolutionary genetics and, 418, 422
Epidemics
poliovirus and, 5
Epidemiology
cat-scratch disease and, 709–10
evolutionary genetics and, 401–2, 404, 420–21
live attenuated varicella vaccine and, 63–64
nucleic acid amplification and, 363–64
Epithelial mucosa
oral bacteria adhesion mechanisms and, 513
Epitopes
tuberculosis pathogenesis and, 259, 270, 272–74
Epoxyqueosine reductase
cobalamin synthesis and use, 146
Epstein-Barr virus (EBV)
nucleic acid amplification and, 352
Epulopiscium fishelsoni
bacterial cell size and, 342–43
Error avoidance systems
spontaneous mutators and, 628–31
Erwinia amylovora
capsular polysaccharide production and, 290, 296
Erwinia carotovora
LuxR-LuxI type regulation and, 730, 732–33, 744
Erwinia chrysanthemi)
pectinolysis and, 213–50
Erwinia spp.
LuxR-LuxI type regulation and, 728, 746
rhizobacterial osmoadaptation and, 102
Erwinia stewartii
capsular polysaccharide

production and, 287, 290, 296
LuxR-LuxI type regulation and, 733, 743
esa genes
LuxR-LuxI type regulation and, 741
Escherichia blattae
cobalamin synthesis and use, 172
Escherichia coli
bacterial cell size and, 319, 322, 324, 327–29, 331, 341
capsular polysaccharide production and, 287–306
cobalamin synthesis and use, 144, 146–47, 154, 160–62, 165, 172–73
evolutionary genetics and, 404, 412, 417, 421
F_0F_1-ATPases and, 791, 793–96, 799, 801–2, 806–7, 809–10, 812–13
genetically engineered synthesis and, 472
heavy metal resistances and, 755, 765–67, 770, 778, 781 β-ketoadipate pathway and, 570, 580–81
LuxR-LuxI type regulation and, 730–31, 733, 735, 739, 745
mycoplasmal molecular biology and, 26–27, 30, 33, 36–37, 44–45
polysaccharide hydrolysis and, 192
rhizobacterial osmoadaptation and, 103, 108–11, 114–15, 117–22, 128
rRNA transcription in
cis and *trans*-acting contributors to rRNA transcription, 649–56
cis-acting requirements for growth rate dependent control, 663
core promoters, 649–51
DNA curvature and rRNA promoter function, 656
feedback mechanism, 664–65, 670
FIS-dependent activation, 653–56
future research, 669–70
growth rate-dependent regulation of rRNA transcription, 662–70
introduction, 646–48
models for growth rate-dependent control, 664–68, 670
(p)ppGpp, 656–60, 665–67
Nus factors, 660–62
overview, 649
passive models for growth rate-dependent control, 667–68
regulatory mechanism compensation, 668–69
UP element, 651–53
spontaneous mutators and, 626–36
Escherichia fergusonii
cobalamin synthesis and use, 172
Escherichia spp.
rhizobacterial osmoadaptation and, 119
Eskimos
poliovirus and, 4
Ethanolamine
cobalamin synthesis and use, 138, 168
Ethanolamine ammonia lyase
cobalamin synthesis and use, 144–46
Ether
enteroviruses and, 9
Euglenophyta
microalgal metabolites and, 434, 445
Eukaryotes
bacterial cell size and, 319, 333, 344
capsular polysaccharide production and, 308
evolutionary genetics and, 401–2, 408
genetically engineered synthesis and, 471
G. lamblia and, 679–702
β-ketoadipate pathway and, 557–58, 565–66
Euplotes crassus
microalgal metabolites and, 448
Euplotes spp.
microalgal metabolites and, 446
Euprymna scolopes
Vibrio fischeri and, 591–618
eut operon
cobalamin synthesis and use, 156, 168–69
Evolution
bacterial cell size and, 320–23
cobalamin synthesis and use, 138, 142
G. lamblia and, 679–84
β-ketoadipate pathway and, 553
Evolutionary clonality
evolutionary genetics and, 419
Evolutionary genetics
bacterial data, 417
better defining question under study, 420–21
data weighting and avoidance of type II statistical error, 419–20
different classes of genetic markers for different uses, 421–22
distinguishing long-term clonal evolution from epidemic clonality, 419
distinguishing long-term clonal evolution from speciation, 418–19
epidemiology, 420–21
glossary, 423–26
goals and tools, 404–5
fungi, 416
links between genetic and biological diversity, 413, 415
numerical methods, 410
paradigm of clonal model, 412–13
parasitic protozoa, 414–16
phylogenetic analysis, 410–11, 413–14, 421
population structure and strain typing, 412–13, 418–20, 422
principles and methods of microbial population genetics, 406–10
taxonomical inferences, 413–14
Trypanosoma cruzi, 412–13
yeasts, 416
HIV/AIDS opportunistic infections, 418
introduction, 402–3
linkage disequilibrium does not amount to clonality, 418–19
selection impact, 418
setting molecular clock, 421–22
Evolutionary snapshot
evolutionary genetics and, 406
Evolved permease system
bacterial cell size and, 332
Exonucleases
spontaneous mutators and, 628–29, 634
Exopolysaccharides
rhizobacterial osmoadaptation and, 107, 129
exp genes
G. lamblia and, 681–82, 688, 690–700

Extracellular polysaccharide (EPS)
capsular polysaccharide production and, 285–86
Extrachromosomal DNA
mycoplasmas and, 32
exu-uxa-uxu genes
pectinolysis regulation in *E. chrysanthemi* and, 236
exuT transport system
pectinolysis regulation in *E. chrysanthemi* and, 223

F

F_0F_1-ATPases
ATP synthases of bacteria (F_0F_1 and A_0A_1, 792–93
coupling of ion translocation to ATP synthesis, 810–14
E. coli F_0F_1, 793–95
F_0 complex structure
organization of subunits *a, b,* and *c* in F_0 complex, 801–4
topology of F_0 subunits, 795–801
introduction, 792–95
molecular mechanism of ion translocation, 804–10
Face
G. lamblia and, 686
Facultative oligotrophs
bacterial cell size and, 333
Families
polysaccharide hydrolysis and, 183, 187–90
Fapy glycosylase
spontaneous mutators and, 630
Faulkner strain
enteroviruses and, 12
Febrile illness
acute
nucleic acid amplification and, 356–57
Feces
coxsackieviruses in, 7
polioviruses in, 2–3, 7
Feedback mechanism
rRNA transcription in *E. coli* and, 645, 664–65, 670
Fermentation
cobalamin synthesis and use, 138, 141–42, 144
Fibrobacter succinogenes
polysaccharide hydrolysis and, 196
Fick's law
bacterial cell size and, 319, 335–37, 339, 343
Filaments
G. lamblia and, 685
FIS-dependent activation
rRNA transcription in *E. coli* and, 653–56
Fish gut bacteria
bacterial cell size and, 342–44
Fitch-Margoliash method
evolutionary genetics and, 410
Fixed heterozygosity
evolutionary genetics and, 412
Flagellation
G. lamblia and, 680–81, 683, 686
Vibrio fischeri-Euprymna scolopes symbiosis and, 602–4
Flies
poliovirus and, 3
Fluorescent antibody
limitations of, 352
Fluoroacetate
halogenated metabolites and, 387–88
Fomites
enteroviruses and, 18
Food chain
microalgal metabolites and, 458–59
Formaldehyde
enteroviruses and, 9
Frateuria spp.
β-ketoadipate pathway and, 563
Frown
G. lamblia and, 686
Fumarate
cobalamin synthesis and use, 138
Fungi
evolutionary genetics and, 402, 416
host penetration and, 491–508
nucleic acid amplification and, 351
Funneling pathways
β-ketoadipate pathway and, 558–60
Fusobacterium spp.
oral bacteria adhesion mechanisms and, 538–39

G

GAG codon
spontaneous mutators and, 627
Galacturonate
pectinolysis regulation in *E. chrysanthemi* and, 225
galE gene
capsular polysaccharide production and, 297
Gamma globulin
poliovirus and, 5
Gambierdiscus toxicus
microalgal metabolites and, 437–39, 458
Gastrointestinal disease
nucleic acid amplification and, 361–62
Generalist markers
evolutionary genetics and, 421–422
Gene clusters
capsular polysaccharide production and, 290–97, 304–6
Gene shuffling
evolutionary genetics and, 408
Genetic distance
evolutionary genetics and, 424
Genetic divergence
evolutionary genetics and, 411
Genetic diversity
bacterial cell size and, 344
capsular polysaccharide production and, 306–8
evolutionary genetics and, 404–5, 413, 415, 422–23
Genetic drift
evolutionary genetics and, 417
Genetic engineering, of natural products
biosynthetic genes, 482–87
carbohydrate synthesis and catabolism
CDP-D-abequose and sialyl T-antigen synthesis, 474, 476
in vitro catabolic pathway construction, 476–77
sequential three and four substrate aldol reactions catalyzed by aldolases, 472–75
cobalamin, 482–87
cofactor regeneration, 469
acyl coenzyme A, 470
nicotinamide cofactors, 470
nucleoside triphosphates, 470
3′-phosphoadenosine-5′-phosphosulfate, 471
S-adenosyl methionine, 471
enzymatic synthesis of bacterial polyketides, 479–82
heme, 482–87
heterologous system, 482–87
hydrogenobyrinic acid, 482–87
introduction, 468–69
multienzyme synthesis exemplified, 472–77

plant secondary metabolites
indole alkaloids, 478–79
isoquinoline alkaloids, 477–78
synthetic design, 471–72
Genetic markers
evolutionary genetics and, 408, 421–22
Genetic photocopy
evolutionary genetics and, 407
Genetic recombination
mycoplasmas and, 37–40
Gene transfer
mycoplasmas and, 40–45
Vibrio fischeri-Euprymna scolopes symbiosis and, 610
Genome
mycoplasmas and, 28–30
Genotype
evolutionary genetics and, 401, 409, 414–15, 418–19, 420–22
Giardia duodenalis
evolutionary genetics and, 414
Giardia lamblia
antigeninc switching of TSA 417 after excystation, 700
cysteine-rich nature of variant surface proteins, 695–96
cysteine-rich proteins define constitutive transport pathway to plasmalemma, 694–95
disease, 681
divergence of constitutive and regulated transport pathways, 700
as early diverging eukaryote, 682–84
evolution of endomembrane transport system, 682–84
exploitation of host stimuli for differentiation, 682
future research, 700–2
introduction, 680
life cycle, 681–82
lysosomal transport pathway, 698
metal binding of variant surface proteins, 697
protease resistance of TSA 417, 696–97
protein transport, 694–700
regulation pathway of protein export to cyst wall during encystation, 698–700
TSA 417 processing and constitutive pathway of protein transport to plasma membrane, 697–98
ultrastructure
anatomy of encystation and excystation, 688, 690–94
axonemes, 686
basal bodies, 686
cell biology of excystation, 694
constitutive endomembranes, 687–89
cytoplasmic domains, 687
cytoskeletal proteins, 686–87
disc proteins, 685
encystation-specific secretory vesicles, 692–94
flagella, 686
general structure, 684–85
median bodies, 686
nuclei, 685
peripheral vacuoles, 687
ventral adhesive disc, 685–87
Giardia muris
G. lamblia and, 687
Giardins
G. lamblia and, 685
Glucans
periplasmic
rhizobacterial osmoadaptation and, 102, 118–22
Glucocorticoids
tuberculosis pathogenesis and, 276–78
Glucose phosphate isomerase
evolutionary genetics and, 412
Glucosylglycerol
rhizobacterial osmoadaptation and, 114
Glucuronate
pectinolysis regulation in *E. chrysanthemi* and, 225
Glutamate
rhizobacterial osmoadaptation and, 108, 110–12
β-1,4-Glycanases
polysaccharide hydrolysis and, 183
Glycerol
cobalamin synthesis and use, 138
Glycerol dehydratase
cobalamin synthesis and use, 146
Glycine betaine
rhizobacterial osmoadaptation and, 108, 110–11, 114–15, 117–18
Glycolipids
tuberculosis pathogenesis and, 263–64
Glycoside hydrolases
polysaccharide hydrolysis and, 192
Glycosylation
G. lamblia and, 683
GlyV locus
spontaneous mutators and, 632
Golgi apparatus
G. lamblia and, 679, 680, 683, 684
Goniodoma spp.
microalgal metabolites and, 440, 442
Gonyaulax spp.
microalgal metabolites and, 435
Gonyautoxin
microalgal metabolites and, 435, 436
GO system
for oxidative repair
spontaneous mutators and, 630–31
G proteins
capsular polysaccharide production and, 292
Grahamella spp.
cat-scratch disease and, 719
Gram-negative bacteria
capsular polysaccharide production and, 290–304
β-ketoadipate pathway and, 556
LuxR-LuxI type regulation and, 728
mycoplasmal molecular biology and, 34
rhizobacterial osmoadaptation and, 108, 112, 129
Gram-positive bacteria
capsular polysaccharide production and, 304–6
mycoplasmal molecular biology and, 27, 34
GroE gene
Vibrio fischeri-Euprymna scolopes symbiosis and, 602
Growth
E. coli and, 645–70
G. lamblia and, 694–700
Vibrio fischeri-Euprymna scolopes symbiosis and, 601
g test
evolutionary genetics and, 408
gutQ gene
capsular polysaccharide production and, 299–300
Gymnodinium breve
microalgal metabolites and, 437–38, 458

Gymnodinium catenatum
microalgal metabolites and, 455, 457
Gymnodinium spp.
microalgal metabolites and, 435, 440, 442

H

Haemophilus ducreyi
nucleic acid amplification and, 352, 360–61
Haemophilus influenzae
capsular polysaccharide production and, 287, 290, 295–302, 307
evolutionary genetics and, 417
heavy metal resistances and, 755
nucleic acid amplification and, 359
HAI-1
LuxR-LuxI type regulation and, 744
HAI-2
LuxR-LuxI type regulation and, 744
Hairpin
cobalamin synthesis and use, 165
H&E stain
limitations of, 352
Halimeda spp.
microalgal metabolites and, 446, 448
Halogenation
biosynthesis of halometabolites
chloramphenicol biosynthesis, 386–87
7-chlorotetracycline biosynthesis, 384–85
fluoroacetate biosynthesis, 387–88
pyrrolnitrin biosynthesis, 387
halogenating enzymes
bacterial haloperoxidases, 389–90
bacterial haloperoxidases and formation of halometabolites, 391–92
heme-containing haloperoxidases, 388–89
in biotechnology, 393–94
vanadium-containing nonheme haloperoxidases, 389
halogenation and dehalogenation, 393
halometabolite-producing bacteria and biological significance of halometabolites
diversity of producing bacteria and biological significance, 382–83
influence of halide ions, 383–84
introduction, 376–77
structural diversity of bacterial halometabolites, 377–82
Hantavirus
nucleic acid amplification and, 352
Haploidy
evolutionary genetics and, 408, 424
Haptophyceae
microalgal metabolites and, 439
Haptophyta
microalgal metabolites and, 434
Hardy-Weinberg equilibrium
evolutionary genetics and, 408, 412–13, 424, 426
HB_{12} propanediol
cobalamin synthesis and use, 138
Heavy metal resistances
arsenic resistance
arsenate reductase enzyme, 769–70
arsenite efflux ATPase, 768–69
molecular genetics of arsenic and antimony resistance, 766–68
bacterial cadmium resistance and genes for human copper transport
CadA Cd^{2+} ATPase of gram-positive bacteria, 757–58
cadmium resistance in *Alcaligenes*, 761
Menkes disease, 758
three-polypeptide chemiosmotic antiporter, 761–62
Wilson's disease, 758–61
cation resistance systems, 781
chromate resistance, 780–81
copper resistance determinants
CopA and CopB ATPases of *E. hirae*, 762–64
Cop of *P. syringae*, 764–65
Pco and Cut of *E. coli*, 765–66
future research, 782
introduction and overview, 754–57
mercury and organomercurial resistances
diversity of operon structure, 770–73
mercuric reductase, 774–76
organomercurial lyase, 774–76
regulatory genes, 776–77
resistance genes in polluted environments, 778
transport, 773–74
metallothionein in cyanobacteria, 778–80
silver resistance, 781
tellurite resistance, 781–82
thallous resistance, 781
HeLa cells
coxsackieviruses and, 15
Heme
cobalamin synthesis and use, 138, 140–41
genetically engineered synthesis and, 482–87
halogenated metabolites and, 388–89
Heparnavirus
discovery and classification of, 20
Hepatitis
nucleic acid amplification and, 361–62
Hepatitis C virus (HCV)
nucleic acid amplification and, 352
Hepatovirus
discovery and classification of, 20
Herpes B virus
nucleic acid amplification and, 351
Herpes zoster
live attenuated varicella vaccine and, 60, 64, 71–73, 77–78
Heterochromatin
G. lamblia and, 685
Heterologous system
genetically engineered synthesis and, 467, 482–87
Heterophile antibody
nucleic acid amplification and, 352
Heterotrophs
bacterial cell size and, 344
Heterozygosity
evolutionary genetics and, 408, 412, 424
H factor
capsular polysaccharide production and, 289
Histoplasma capsulatum
nucleic acid amplification and, 356
Histoplasmosis

nucleic acid amplification and, 352
HNS protein
pectinolysis regulation in *E. chrysanthemi* and, 214
Homologous expression
genetically engineered synthesis and, 467
Homologous recombination
capsular polysaccharide production and, 307
Homologous recombination
mycoplasmas and, 38
Homologous repair systems
spontaneous mutators and, 626
Homoplasy
evolutionary genetics and, 411, 423–24, 426
Homo sapiens
evolutionary genetics and, 404
Homostachydrine
rhizobacterial osmoadaptation and, 124
Hosmotic adaptation
rhizobacterial osmoadaptation and, 101
Host development program
Vibrio fischeri-Euprymna scolopes symbiosis and, 604–7
Host penetration
M. grisea and, 491–508
Host responses
Vibrio fischeri-Euprymna scolopes symbiosis and, 604–7
Host stimuli
G. lamblia and, 682
hrpM gene
rhizobacterial osmoadaptation and, 127
hsd genes
mycoplasmal molecular biology and, 40, 43–44
Human embryonic kidney (HEK) cells
enteroviruses and, 14
Human immunodeficiency virus (HIV)
analysis of virologic and immunologic events associated with advanced stage disease
immunologic events, 849
virologic events, 848–49
analysis of virologic and immunologic events associated with clinically latent period of HIV disease
immunologic events, 846–48
virologic events, 844–45
analysis of virologic and immunologic events associated with primary HIV infection
virologic events, 831–40
clinical course of HIV infection, 828–29
evolutionary genetics and, 416, 418
introduction, 826–27, 848
long-term nonprogressors, 830–31
long-term survivors, 831
nucleic acid amplification and, 352
potential mechanisms responsible for failure of primary immune response to eliminate HIV, 840–44
rapid progressors, 830
tuberculosis pathogenesis and, 260
typical progressors, 828, 830
Humoral immunity
live attenuated varicella vaccine and, 73
Hybridoma technology
nucleic acid amplification and, 349
Hydrogenobyrinic acid
genetically engineered synthesis and, 482–87
Hydrolysis
microbial
polysaccharides and, 183–204
4-Hydroxybenzoate
β-ketoadipate pathway and, 553, 569–72
Hypercalcemia
tuberculosis pathogenesis and, 275
Hypersensitive response
LuxR-LuxI type regulation and, 745
Hypoosmotic adaptation
rhizobacterial osmoadaptation and, 118–22

I

I^-
halogenated metabolites and, 375
IEM
G. lamblia and, 679
Illegitimate recombination
mycoplasmas and, 40
Immunoassays
nucleic acid amplification and, 349
Immunocompromised individuals
live attenuated varicella vaccine and, 60, 64, 83–84
Immunologic events
HIV mechanisms of disease and, 825, 831, 835–44, 846–49
live attenuated varicella vaccine and, 81, 82
tuberculosis pathogenesis and, 259, 261, 265–76, 279
Indirect fluorescent assay (IFA)
cat-scratch disease and, 716–18, 721
Indole alkaloids
genetically engineered synthesis and, 478–79
Infections
invasive
capsular polysaccharide production and, 285
persistent
nucleic acid amplification and, 357–58
Infectious disease
nucleic acid amplification and, 349, 363–64
Influenza
poliovirus and, 6
Insertion sequence elements
mycoplasmal molecular biology and, 28, 31
Intercellular signaling
LuxR-LuxI type regulation and, 744–45
Internally limited growth rate
bacterial cell size and, 332
Intracellular signaling
LuxR-LuxI type regulation and, 744–45
Intraspecies mating
mycoplasmas and, 42
'Introns early' model
bacterial cell size and, 323
In vitro multienzyme synthesis
genetically engineered synthesis and, 467
Ion translocation
F_0F_1-ATPases and, 804–14
Iron deprivation
pectinolysis regulation in *E. chrysanthemi* and, 214, 233–34
Iron sequestration
Vibrio fischeri-Euprymna scolopes symbiosis and, 615
Isoenzymes

evolutionary genetics and, 410–13, 424–25
Isoquinoline alkaloids
genetically engineered synthesis and, 477–78
Isozymes
β-ketoadipate pathway and, 553, 573–74

J

Japan
live attenuated varicella vaccine and, 78–79

K

K^+
rhizobacterial osmoadaptation and, 108, 110, 112, 122
K antigens
capsular polysaccharide production and, 286–87, 289–96
KatF locus
spontaneous mutators and, 629
KDG kinase
pectinolysis regulation in *E. chrysanthemi* and, 224
KDG oxidoreductase
pectinolysis regulation in *E. chrysanthemi* and, 224
KDGP-aldolase
pectinolysis regulation in *E. chrysanthemi* and, 224–25
Kdgr regulon
pectinolysis regulation in *E. chrysanthemi* and, 214, 236–41
kdgT transport system
pectinolysis regulation in *E. chrysanthemi* and, 223
kdp genes
rhizobacterial osmoadaptation and, 109
kds genes
capsular polysaccharide production and, 302
β-Ketoadipate pathway
biological distribution
eukaryotes, 558
funneling pathways, 558–60
prokaryotes, 556, 558
conservation of enzyme structure and function
chemotaxis, 568–72
eukaryotes, 565–66
4-hydroxybenzoate, 569–72
β-ketoadipate transport, 572–73
PcaK protein, 569–72
prokaryotes, 559, 561–65
relationship to modified *ortho* pathways, 566–68
transport, 569–72
introduction, 554–57
pathway organization and regulation in diverse bacteria
branch convergence and isozymes, 573–74
communication between branches, 581–82
gene organization, 575, 577
inducing metabolites, 575–76
regulators and operons, 579–81
supraoperonic clustering, 575–79
selection forces shaping self-identity, 582–83
kfi genes
capsular polysaccharide production and, 293, 303–4
Klebsiella pneumoniae
capsular polysaccharide production and, 290, 296
F_0F_1-ATPases and, 810
polysaccharide hydrolysis and, 193
Klebsiella spp.
capsular polysaccharide production and, 291, 304
cobalamin synthesis and use, 172
Koch phenomenon
tuberculosis pathogenesis and, 259, 261, 266–67, 271–72, 276–77
kps genes
capsular polysaccharide production and, 294–95, 298–302, 307
kup gene
rhizobacterial osmoadaptation and, 109
K-variants
Vibrio fischeri-Euprymna scolopes symbiosis and, 604

L

Lac^+
spontaneous mutators and, 626–27, 636–38
Lactone
cobalamin synthesis and use, 152
lacZ operon
rhizobacterial osmoadaptation and, 128
spontaneous mutators and, 627
las genes
LuxR-LuxI type regulation and, 743
Last universal ancestor
bacterial cell size and, 320–21
Latency
HIV mechanisms of disease and, 844–45
live attenuated varicella vaccine and, 60, 67–68
Legionella pneumophila
cat-scratch disease and, 714
evolutionary genetics and, 417
Legionella spp.
nucleic acid amplification and, 351–52, 356
Legumes
rhizobacterial osmoadaptation and, 123–26
Leishmania amazonensis
evolutionary genetics and, 412
Leishmania brasiliensis
evolutionary genetics and, 412–14
Leishmania chagasi
evolutionary genetics and, 412, 414
Leishmania donovani
evolutionary genetics and, 414
Leishmania guyanensis
evolutionary genetics and, 406, 413
Leishmania infantum
evolutionary genetics and, 412, 414
Leishmania mexicana
evolutionary genetics and, 414
Leishmania panamensis
evolutionary genetics and, 406
Leishmania spp.
evolutionary genetics and, 408, 414, 416, 421
Lepotrichia spp.
cat-scratch disease and, 713
Leukemic vaccines
live attenuated varicella vaccine and, 79–80
Level of resolution
evolutionary genetics and, 401, 421
Life cycle
G. lamblia and, 681–82
Ligase chain reaction (LCR)

nucleic acid amplification and, 353
Light organ
Vibrio fischeri-Euprymna scolopes symbiosis and, 591–18
Lignins
β-ketoadipate pathway and, 553
Lim-Benyesh-Melnick combination antiserum pools
enteroviruses and, 12
Linkage disequilibrium
evolutionary genetics and, 408–9, 411–13, 415–19, 425
lip genes
capsular polysaccharide production and, 297
Lipids
tuberculosis pathogenesis and, 263–64
Lipoarabinomannan (LAM)
tuberculosis pathogenesis and, 264–65
Lipooligosaccharide (LOS)
capsular polysaccharide production and, 285, 297, 307
Lipopolysaccharide (LPS)
capsular polysaccharide production and, 285, 291, 297, 301
rhizobacterial osmoadaptation and, 129
Liquefaction
tuberculosis pathogenesis and, 276–77
Listeria spp.
heavy metal resistances and, 757
Locus
evolutionary genetics and, 408, 425
lpsZ gene
capsular polysaccharide production and, 301
Luminescence
Vibrio fischeri-Euprymna scolopes symbiosis and, 591, 601–2, 614–15
Lupus vulgaris
tuberculosis pathogenesis and, 267
LuxR-LuxI type regulation
autoinducer biosynthesis, 731, 735–37
cis-acting promoter elements, 740–41
in diverse bacteria, 730–36
ecology of quorum-sensing bacteria, 743–44
future research, 745–46
integrated model for quorum sensing
additional component of *A. tumefaciens* quorum sensor, 742
quorum-sensing modules as components of regulatory cascades, 742–43
introduction, 728–29
LuxR-type proteins, 737
as autoinducer receptors, 738–40
multimerization of LuxR, 740
regulatory gene arrangement, 741
related systems of intracellular and intercellular signaling, 744–45
functions outside of quorum sensing, 745
other quorum-sensing systems, 745
Lyme disease
nucleic acid amplification and, 352
Lyngbya majuscula
microalgal metabolites and, 440–41, 443, 445, 458
Lyngbya wollei
microalgal metabolites and, 436, 455
Lysogenic mycoplasma viruses
site-specific recombination and, 38
Lysosomal transport pathway
G. lamblia and, 698
LysR transcriptional regulators
pectinolysis regulation in *E. chrysanthemi* and, 214

M

Macrolides
microalgal metabolites and, 439–40
Macrophages
tuberculosis pathogenesis and, 264–65, 276
Magnaporthe grisea
extracellular enzymes in penetration, 506–7
genetic production of melanin production and deficiency, 501–2
infection structures
appressoria, 495–98
conidia, 493–95
melanization and appressorium pore, 498–99
penetration pegs, 498–501
spore tip mucilage, 495
introduction, 492
mechanical forces in penetration, 502
appressorial turgor pressure, 503–6
Maize roots
rhizobacterial osmoadaptation and, 106–7
Major histocompatibility complex (MHC) class 1
tuberculosis pathogenesis and, 262–63
Mandelate
β-ketoadipate pathway and, 564
Marasmus
coxsackieviruses and, 16
Mating
mycoplasmas and, 42–43
Matric potential
rhizobacterial osmoadaptation and, 104–5
mdo genes
rhizobacterial osmoadaptation and, 121
mecA gene
nucleic acid amplification and, 363
Median bodies
G. lamblia and, 686
Medicine
evolutionary genetics and, 402
Melanin
M. grisea and, 491, 498–99, 501–2
Melnick, J.L., 1–20
Membrane-derived oligosaccharides
rhizobacterial osmoadaptation and, 119
Meningitis
nucleic acid amplification and, 359
Menkes disease
heavy metal resistances and, 758–61
Mercuric reductase
heavy metal resistances and, 774–76
Mercury
heavy metal resistances and, 755, 770–73
Mesoplasma florum
mycoplasmal molecular biology and, 29
Mesoplasma lactucae
mycoplasmal molecular biology

and, 29
Mesoplasma spp.
mycoplasmal molecular biology and, 28
Messenger RNA (mRNA)
bacterial cell size and, 329, 338
cobalamin synthesis and use, 165–66
Metabolism
bacterial cell size and, 332, 340–42
cobalamin synthesis and use, 138
β-ketoadipate pathway and, 575–76
tuberculosis pathogenesis and, 275–77
Metabolites
halogenated, 375–94
microalgal, 431–59
plant secondary, 477–79
meta-cleavage pathways
β-ketoadipate pathway and, 555–56
Metal binding
G. lamblia and, 697
Metal ions
toxic
heavy metal resistances and, 753–82
Metallothionein
heavy metal resistances and, 778–80
met genes
cobalamin synthesis and use, 149–50, 154, 159–60, 166
Methane
cobalamin synthesis and use, 147
Methanobacterium spp.
microalgal metabolites and, 435
Methionine synthetase
cobalamin synthesis and use, 146
Methyl transfer
cobalamin synthesis and use, 147
miaA gene
spontaneous mutators and, 634
Michaelis-Menten type isotherm
bacterial cell size and, 335
Microalgal metabolites
biosynthesis, 446–47
miscellaneous algal metabolites, 454
nitrogenous compounds, 447–49
polyketides, 449, 451–54
cyclic oxylipins or eicosanoids, 441–42
food chain, 458–59
genetics of secondary metabolites and symbionts' role, 454–58
introduction, 432–35
macrolides, 439–40
miscellaneous compounds, 443, 445–46
open-chain polyketides, 440–41
peptides, 443
polyether compounds, 436–38
saxitonin and gonyautoxin derivatives, 435–36
sterols and related compounds in membranes, 433
Microbispora bispora
polysaccharide hydrolysis and, 201
Microcystis spp.
microalgal metabolites and, 449
Micromonospora echinospora
halogenated metabolites and, 380
Microscopy
limitations of, 352
Minicells
bacterial cell size and, 340
Mismatch repair
bacterial cell size and, 326
spontaneous mutators and, 628–29
Modification systems
mycoplasmas and, 43–44
Molecular clocks
evolutionary genetics and, 401, 405, 420–22
Molecular genetic approaches
Vibrio fischeri-Euprymna scolopes symbiosis and, 609–12
Molecular pathogenesis
mycoplasmas and, 45–48
Molecular susceptibility testing
nucleic acid amplification and, 362–63
Mollicutes
mycoplasmal molecular biology and, 26, 29, 41
Monod model
bacterial cell size and, 332
Monte Carlo techniques
bacterial cell size and, 339
Moraxella spp.
microalgal metabolites and, 455
Morganella morganii
cobalamin synthesis and use, 172
Motility
Vibrio fischeri-Euprymna scolopes symbiosis and, 612–14
Motility-associated contractile proteins
G. lamblia and, 686–87
Mucigel
rhizobacterial osmoadaptation and, 128–29
Multienzyme synthesis
genetically engineered synthesis and, 472–77
Multilocus enzyme electrophoresis (MLEE)
evolutionary genetics and, 409, 411–13, 415, 417, 420–21, 425
Multimerization
LuxR-LuxI type regulation and, 740
Multiple sequence alignments
LuxR-LuxI type regulation and, 734–35
Mumps
poliovirus and, 6
Murein
bacterial cell size and, 323–25
rhizobacterial osmoadaptation and, 129
Murex brandaris
halogenated metabolites and, 377
Murex spp.
halogenated metabolites and, 376
Mus musculus
evolutionary genetics and, 404
Mutagenesis
spontaneous mutators and, 625–39
Vibrio fischeri-Euprymna scolopes symbiosis and, 591, 611
mut genes
spontaneous mutators and, 628–38
MV strain
poliovirus, 4
Mycobacterium avium
tuberculosis pathogenesis and, 275
Mycobacterium avium-intracellulare
nucleic acid amplification and, 356
Mycobacterium bovis
evolutionary genetics and, 414
tuberculosis pathogenesis and, 259, 262, 276
Mycobacterium kansasii
nucleic acid amplification and, 356

Mycobacterium leprae
tuberculosis pathogenesis and, 272
Mycobacterium spp.
nucleic acid amplification and, 352
Mycobacterium tuberculosis
evolutionary genetics and, 414, 422
nucleic acid amplification and, 352, 354–55, 359, 362
tuberculosis pathogenesis and, 261–63, 265–66, 268–74
Mycobacterium vaccae
tuberculosis pathogenesis and, 268–69, 272, 274
Mycoplasma arthritidis
mycoplasmal molecular biology and, 29, 31–32, 39, 41
Mycoplasma bovis
mycoplasmal molecular biology and, 29, 47–48
Mycoplasma buccale
mycoplasmal molecular biology and, 37
Mycoplasma capricolum
mycoplasmal molecular biology and, 28–30, 33, 37, 41, 44
Mycoplasma fermentans
mycoplasmal molecular biology and, 29, 31, 43
Mycoplasma flocculare
mycoplasmal molecular biology and, 29
Mycoplasma gallisepticum
mycoplasmal molecular biology and, 29, 31, 37–39, 41, 45
Mycoplasma genitalium
mycoplasmal molecular biology and, 28–31, 33–34, 36–37, 43, 45, 48
Mycoplasma hominis
mycoplasmal molecular biology and, 29, 31, 39, 42–43
Mycoplasma hyopneumoniae
mycoplasmal molecular biology and, 29–31, 33
Mycoplasma hyorhinis
mycoplasmal molecular biology and, 29, 31, 46–47
Mycoplasma iowae
mycoplasmal molecular biology and, 29–30
Mycoplasma mobile
mycoplasmal molecular biology and, 29, 45
Mycoplasma mycoides
mycoplasmal molecular biology and, 28–32, 39–41, 44
Mycoplasma pneumoniae
mycoplasmal molecular biology and, 29–33, 35, 37, 39, 41, 43, 45–48
nucleic acid amplification and, 356
Mycoplasma pulmonis
mycoplasmal molecular biology and, 29, 31–32, 36, 38–40, 42–48
Mycoplasma salivarium
mycoplasmal molecular biology and, 29, 42
Mycoplasma spp.
mycoplasmal molecular biology and, 28, 32, 36, 42, 44
Mycoplasmas
chromosome replication and repair
DNA repair, 37
DNA replication, 35–37
enteroviruses and, 14
extrachromosomal DNA, 32
gene transfer
cloning vectors, 44–45
conjugal transfer of TN*916*, 42–43
intraspecies mating, 42
mating, 42–43
modification systems, 43–44
restriction systems, 43–44
selectable markers, 40–41
transformation, 41–42
genetic recombination, 37
homologous recombination, 38
illegitimate recombination, 40
lysogenic mycoplasma viruses, 38
site-specific DNA inversion, 39–40
site-specific recombination, 38–40
genetic recombination, transposable elements, 38–39
genome size and base composition, 28–30
genomic sequence analysis, 30–31
introduction, 26–27
molecular pathogenesis, adhesion, 45–46
molecular pathogenesis, antigenic and pahase variation mechanisms, 46–48
phylogeny, 27–28
protein production
posttranslational modification, 35
transcription, 33
translation, 33–34
repetitive elements, 31–32
taxonomy, 27–28
Myxobacteria
bacterial cell size and, 328
Myxococcus fulvus
halogenated metabolites and, 378
Myxococcus spp.
halogenated metabolites and, 383, 387
Myxococcus xanthus
LuxR-LuxI type regulation and, 728, 745

N

Na^+
rhizobacterial osmoadaptation and, 104
N-acetylglutaminylglutamine amide (NAGGN)
rhizobacterial osmoadaptation and, 111, 113
NADH
genetically engineered synthesis and, 470
NADPH
genetically engineered synthesis and, 470
Nanobacteria
bacterial cell size and, 340
Natural products
genetically engineered synthesis and, 467–87
Natural selection
β-ketoadipate pathway and, 553
ndv genes
rhizobacterial osmoadaptation and, 120–22, 125–26
Necrosis
tuberculosis pathogenesis and, 259, 261, 266–67, 274, 276
Neisseria gonorrhoeae
evolutionary genetics and, 417–18
nucleic acid amplification and, 351, 360
Neisseria meningitidis
capsular polysaccharide production and, 287, 289–90, 295–302, 303, 307
evolutionary genetics and, 417–18
Neocallimastix frontalis
polysaccharide hydrolysis and, 197

Neocallimastix patriciarum
polysaccharide hydrolysis and, 197
neuA gene
capsular polysaccharide production and, 307
Neurospora crassa
F_0F_1-ATPases and, 798
β-ketoadipate pathway and, 558, 566
Neurospora spp.
heavy metal resistances and, 778
nfo gene
spontaneous mutators and, 634
Nitrate
cobalamin synthesis and use, 138
Nitrate reductases
cobalamin synthesis and use, 140
Nitric oxide
tuberculosis pathogenesis and, 264
Nitrogen
pectinolysis regulation in *E. chrysanthemi* and, 232–33
Nitrogenase
rhizobacterial osmoadaptation and, 123
Nitrogenous compounds
microalgal metabolites and, 447–49
Nitzschia pungens
microalgal metabolites and, 443, 458
Nocardia erythropolis
β-ketoadipate pathway and, 562
Nocardia spp.
halogenated metabolites and, 383
β-ketoadipate pathway and, 556, 576
Nodularia spp.
microalgal metabolites and, 449
Nodulation
capsular polysaccharide production and, 290
rhizobacterial osmoadaptation and, 123–25
Nonspecific host immunity
capsular polysaccharide production and, 287–89
Nuclear pyknosis
enteroviruses and, 14
Nuclei
G. lamblia and, 685
Nucleic acid amplification
central nervous system disease
encephalitis, 359
meningitis, 359
conventional clinical microbiology, 351–52
gastrointestinal disease
hepatitis, 361–62
Whipple's-associated bacillus, 362
infectious disease epidemiology, 363–64
introduction, 350–51
limitations of current methods in diagnostic microbiology, 352
molecular susceptibility testing, 362–63
overview, 352–54
respiratory diseases
atypical pneumonia, 355–56
Mycobacterium tuberculosis, 354–55
streptococcal pharyngitis, 355
systemic disease
acute febrile illness, 356–57
persistent infections, 357–58
urogenital infection
cervicitis, 360
ulcerative disease, 360–61
urethritis, 360
Nucleic acid sequence based amplification (NASBA) methodology and, 353
Nucleoside triphosphates (NTPs)
genetically engineered synthesis and, 470
Nus factors
E. coli and, 660–62
Nutritional deprivation
bacterial cell size and, 327–28

O

ogt ada double mutant
spontaneous mutators and, 634
Oka strain
live attenuated varicella vaccine and, 60, 62, 78
Olfactory nerves
poliovirus and, 3
Oligobacteria
bacterial cell size and, 340
Oligogalacturonate lyase
pectinolysis regulation in *E. chrysanthemi* and, 219–20
Oligogalacturonides
pectinolysis regulation in *E. chrysanthemi* and, 214
Oligotrophs
bacterial cell size and, 331, 333, 340–41
Open reading frames (ORFs)
capsular polysaccharide production and, 305
Operons
β-ketoadipate pathway and, 579–81
Opportunistic infections
evolutionary genetics and, 418–19
Opsonophagocytosis
capsular polysaccharide production and, 288–89
Oral bacteria adhesion mechanisms
actinomyces adherence, 533–37
bacterial communication, 542–43
Captnocytophaga adherence, 540
fusobacterium adherence, 538–39
introduction, 514–15
invasion, 540–41
Actinobacillus actinomycetemcomitans, 542
Porphromonas gingivalis, 541–42
Treponema denticola, 541
pellicle receptors, 519–20
population composition changes, 516–17
Porphyromonas adherence, 537–38
Prevotella adherence, 537
salivary proteins, 519–20
streptococcal adherence
adhesins, 523–30
interactions, 520–23
receptors, 530–33
surfaces, occupants, and multiple mechanisms of adherence, 515–16
temporal relationship of subgingival occupants and coaggregation partnerships, 517–19
Treponema adherence, 539–40
Veillonella adherence, 540
Organomercurial lyase
heavy metal resistances and, 774–76
Original uptake capability
bacterial cell size and, 332
Orphan viruses
discovery and classification of, 8–9

ortho-cleavage pathways
  β-ketoadipate pathway and, 553, 555–56, 558–59, 561, 566–68, 579
Oscillatoria morigeotii
  microalgal metabolites and, 436, 455
osmA gene
  rhizobacterial osmoadaptation and, 109
Osmoadaptation
  rhizobacteria and, 101–29
Osmoprotectant uptake
  rhizobacterial osmoadaptation and, 114–17
Osmoregulation
  pectinolysis regulation in *E. chrysanthemi* and, 231–32
Ostreopsis siamensis
  microalgal metabolites and, 441, 444, 459
otsAB operon
  rhizobacterial osmoadaptation and, 109, 110
Overflow metabolism
  bacterial cell size and, 332
Oxidative damage
  spontaneous mutators and, 629–31
Oxidative metabolism
  bacterial cell size and, 342
Oxygen
  cobalamin synthesis and use, 138, 142, 151–53
  pectinolysis regulation in *E. chrysanthemi* and, 214, 232–33
  spontaneous mutators and, 629–31
Oxylipins
  cyclic
    microalgal metabolites and, 441–42
oxyR gene
  spontaneous mutators and, 629, 635

P

p24 antigen
  nucleic acid amplification and, 352
PAI-1
  LuxR-LuxI type regulation and, 740
Palmaria palmata
  microalgal metabolites and, 445
Palythoa spp.
  microalgal metabolites and, 441, 459
Panmictic species
  evolutionary genetics and, 401, 407–8, 410–11, 418–19
Papillation
  spontaneous mutators and, 626–27
Paralysis
  poliovirus and, 3–6, 17–18
Parinaud's oculoglandular syndrome
  cat-scratch disease and, 708, 711, 713
Passive antibody prophylaxis
  live attenuated varicella vaccine and, 75
Pathogenicity
  evolutionary genetics and, 401, 404–5
  M. grisea and, 491–508
  tuberculosis pathogenesis and, 273
Pathway intermediates
  genetically engineered synthesis and, 467
pca genes
  β-ketoadipate pathway and, 561–64, 572, 574–75, 577–81
PcaK protein
  β-ketoadipate pathway and, 569–72
pco genes
  heavy metal resistances and, 765–66
pdu operon
  cobalamin synthesis and use, 150, 156, 168–69
pec genes
  pectinolysis regulation in *E. chrysanthemi* and, 241–44
Pectinolysis, in *Erwinia chrysanthemi*
  introduction, 214–15
  pectin degradation, 215–16
    catabolism of monomers derived from pectin cleavage, 222–25
    contribution of individual pectinases to plant maceration and bacterial virulence, 221–22
    deoxyuronate isomerase, 223–24
    exuT transport system, 223
    galacturonate and glucuronate catabolism steps, 225
    KDG kinase, 224
    KDG oxidoreductase, 224
    KDGP-aldolase, 224–25
    kdgT transport system, 223
    maturation and secretion of pectinases, 220
    oligogalacturonate lyase, 219–20
    pectate lyases, 216–18
    pectin lyase, 219
    pectin methylesterases, 218–19
    polygalacturonase, 219
  regulatory elements, 234–35
    additional regulatory systems, 244–46
    exu-uxa-uxu gene regulation, 236
    KdgR regulon, 236–41
    PecS-PecM regulatory couple, 241–43
    PecT regulator, 243–44
    regulatory sites, 246–48
  stimuli affecting pectinase production, 225–26
    catabolite repression, 229
    expression of pectin genes in planta, 227
    induction by pectin-degradation intermediates, 227–28
    iron deprivation, 233–34
    osmoregulation, 231–32
    other inducers from plant extracts, 228–29
    oxygen and nitrogen availability, 232–33
    pnl regulation by DNA-damaging agents, 234
    stationary phase induction, 229–30
    thermoregulation, 232
pel genes
  pectinolysis regulation in *E. chrysanthemi* and, 214
Pellicle receptors
  oral bacteria adhesion mechanisms and, 519–20
Penetration pegs
  M. grisea and, 498, 500–1
Penicillium griseofulvum
  halogenated metabolites and, 377
Penicillium spp.
  halogenated metabolites and, 376
Peptoglycan
  bacterial cell size and, 323
Peripheral vacuoles
  G. lamblia and, 687

Permease
bacterial cell size and, 331–32, 340
Persisters
tuberculosis pathogenesis and, 261
Pesascek strain
enterovirus, 10
pH
enteroviruses and, 9
G. lamblia and, 682
Phanerochaete chrysosporium
polysaccharide hydrolysis and, 195, 201
Phaeophyta
microalgal metabolites and, 434
Phase variation mechanisms
mycoplasmas and, 46–48
Phenol
enteroviruses and, 9
Phenotype
evolutionary genetics and, 416
spontaneous mutators and, 625, 628
Phormia regina
poliovirus and, 3
Phosphate
cobalamin synthesis and use, 158–59
Vibrio fischeri-Euprymna scolopes symbiosis and, 603
3'-Phosphoadenosine-5'-phosphosulfate (PAPS)
genetically engineered synthesis and, 471
Photorhabdus luminescens
Vibrio fischeri-Euprymna scolopes symbiosis and, 604
Phototrophs
bacterial cell size and, 333
Phylogeny
evolutionary genetics and, 401, 404–6, 409–11, 413–14, 418, 421–22
β-ketoadipate pathway and, 573
mycoplasmal molecular biology and, 34
Phytoremediation
heavy metal resistances and, 776
phz genes
LuxR-LuxI type regulation and, 741
Picobacteria
bacterial cell size and, 340
Picornaviruses
discovery and classification of, 1, 20
Piromyces spp.
polysaccharide hydrolysis and, 197
Plant cell walls
polysaccharide hydrolysis and, 183, 195–201
Plant extracts
pectinolysis regulation in *E. chrysanthemi* and, 214, 228–29
Plant-microbe interactions
rhizobacterial osmoadaptation and, 122–27
Plant secondary metabolites
genetically engineered synthesis and, 477–79
Plasma membrane
G. lamblia and, 684, 687, 694–95, 697
Plasmodium falciparum
evolutionary genetics and, 408, 415–16, 418
Plasmodium spp.
nucleic acid amplification and, 357
Pleiotropic response
Vibrio fischeri-Euprymna scolopes symbiosis and, 604
Plexaura homomalla
microalgal metabolites and, 442
plpA gene
capsular polysaccharide production and, 305
Plumber's model
for rRNA synthesis, 670
Pneumocystis carinii
evolutionary genetics and, 416
Pneumocystis spp.
nucleic acid amplification and, 356
Pneumonia
atypical
nucleic acid amplification and, 355–56
pnl genes
pectinolysis regulation in *E. chrysanthemi* and, 234
pob genes
β-ketoadipate pathway and, 575, 577, 580–81
pocR gene
cobalamin synthesis and use, 162–64
polA gene
spontaneous mutators and, 635
Polioviruses
discovery and classification of, 1–18
Pollution
heavy metal resistances and, 778
Polyether compounds
microalgal metabolites and, 431, 436–38
Polygalacturonase
pectinolysis regulation in *E. chrysanthemi* and, 214, 219
Polyketides
genetically engineered synthesis and, 467, 479–82
microalgal metabolites and, 440–41, 449, 451–54
Polymerase chain reaction (PCR)
capsular polysaccharide production and, 305
cat-scratch disease and, 715
evolutionary genetics and, 416, 418, 422
nucleic acid amplification and, 350, 353, 356–60, 363
Polysaccharide hydrolysis
aerobic microorganisms, 199–201
anaerobic microorganisms, 196–99
chitin-hydrolyzing systems, 193–95
enzyme systems, 192–93
enzyme families, 187–90
glycoside hydrolases, 192
inverting and retaining enzymes, 186–87
substrate-binding domains, 190–92
introduction, 184–85
overview, 201–4
plant cell wall-hydrolyzing systems, 195–201
starch-hydrolyzing systems, 193
substrates, 185–86
Polysaccharides
capsular, 129, 285
rhizobacterial osmoadaptation and, 107
Polyvalence
evolutionary genetics and, 414
Polyvinyl pyrrolidone (PVP)
bacterial cell size and, 334
Population structure
evolutionary genetics and, 411–13, 418–20, 422
Porphyrins
cobalamin synthesis and use, 140
genetically engineered synthesis and, 482–87

Porphyromonas gingivalis
oral bacteria adhesion mechanisms and, 541–42
Porphyromonas spp.
oral bacteria adhesion mechanisms and, 537–38
Posttranslational modification
mycoplasmas and, 35
(p)ppGpp
E. coli and, 656–60, 665–67
Prasinophyta
microalgal metabolites and, 434
Precipitin
enteroviruses and, 12
Precorrin-2
cobalamin synthesis and use, 153
Pressure
M. grisea and, 491, 503–6
Prevotella ruminicola
polysaccharide hydrolysis and, 196
Prevotella spp.
oral bacteria adhesion mechanisms and, 537
Pribnow box
mycoplasmal molecular biology and, 33
Primary infection
HIV mechanisms of disease and, 825, 831–40
Probe amplfication
nucleic acid amplification and, 353
Procentrum lima
microalgal metabolites and, 440
Proctista
microalgal metabolites and, 431–59
Prokaryotes
bacterial cell size and, 317, 319–20, 323–25, 327–28, 333, 341, 344
evolutionary genetics and, 401–2
genetically engineered synthesis and, 471
β-ketoadipate pathway and, 556–59, 561–65
Proline
rhizobacterial osmoadaptation and, 108, 110–13
Proline betaine
rhizobacterial osmoadaptation and, 108, 110–11, 115–16
Promoters
E. coli and, 656
LuxR-LuxI type regulation and, 740–41
rRNA transcription in *E. coli* and, 645, 649–51
Proofreading
spontaneous mutators and, 628
Propanediol
cobalamin synthesis and use, 138, 167–68
Propanediol dehydratase
cobalamin synthesis and use, 144
proP gene
rhizobacterial osmoadaptation and, 109–10
Propionibacterium shermanii
cobalamin synthesis and use, 138, 151, 156
Propionigenium modestum
F_0F_1-ATPases and, 792, 806, 808–11
Prorocentrum concavum
microalgal metabolites and, 437, 458
Prorocentrum lima
microalgal metabolites and, 437, 442, 458
Prosthecate bacteria
bacterial cell size and, 328
Proteases
G. lamblia and, 696–97
Protein export
G. lamblia and, 698–700
Protein synthesis
bacterial cell size and, 317, 321–22, 327, 329
mycoplasmas and, 33–35
Proteus mirabilis
capsular polysaccharide production and, 288
Protocatechuate
β-ketoadipate pathway and, 553, 560
Protozoa
parasitic
evolutionary genetics and, 402, 408, 414–16
proU gene p
rhizobacterial osmoadaptation and, 109–10
Prymnesium parvum
microalgal metabolites and, 439
Pseudomonas aeruginosa
capsular polysaccharide production and, 288
evolutionary genetics and, 417
halogenated metabolites and, 378
heavy metal resistances and, 780
β-ketoadipate pathway and, 561, 573, 578
LuxR-LuxI type regulation and, 728, 730, 732, 739, 741, 743, 746
rhizobacterial osmoadaptation and, 103, 113, 118
Pseudomonas arvilla
β-ketoadipate pathway and, 561, 563
Pseudomonas aurofaciens
LuxR-LuxI type regulation and, 732
Pseudomonas cepacia
halogenated metabolites and, 383
β-ketoadipate pathway and, 575
Pseudomonas denitrificans
cobalamin synthesis and use, 138, 141, 148–53, 155–59, 164–65
Pseudomonas fluorescens
halogenated metabolites and, 378, 383, 387, 392
β-ketoadipate pathway and, 573
polysaccharide hydrolysis and, 199
rhizobacterial osmoadaptation and, 113, 128
Pseudomonas halophila
rhizobacterial osmoadaptation and, 113–14
Pseudomonas halosaccharolytica
rhizobacterial osmoadaptation and, 113–14
Pseudomonas mendocina
rhizobacterial osmoadaptation and, 113–14
Pseudomonas pseudoalcaligenes
rhizobacterial osmoadaptation and, 113–14
Pseudomonas putida
cobalamin synthesis and use, 150, 157
β-ketoadipate pathway and, 553, 559, 561–66, 568–73, 575, 577–82
rhizobacterial osmoadaptation and, 113, 126
Pseudomonas pyrrocinia
halogenated metabolites and, 389–90
Pseudomonas solanacearum
capsular polysaccharide production and, 290, 296
Pseudomonas spp.
capsular polysaccharide production and, 288
halogenated metabolites and, 383, 387, 389

heavy metal resistances and, 772, 778, 780
β-ketoadipate pathway and, 558–59, 574, 576
rhizobacterial osmoadaptation and, 101–2, 107–8, 112–13, 115–16, 119, 126–27
Pseudomonas stutzeri
rhizobacterial osmoadaptation and, 113
Pseudomonas syringae
heavy metal resistances and, 764–65
LuxR-LuxI type regulation and, 745
rhizobacterial osmoadaptation and, 103, 121, 127
Pseudonitzschia pungens
microalgal metabolites and, 442, 454
Pseudonodules
rhizobacterial osmoadaptation and, 125
Pulsed field gel electrophoresis (PFGE)
evolutionary genetics and, 413
nucleic acid amplification and, 363–64
Pumping
heavy metal resistances and, 756
Purified protein derivative anergy
nucleic acid amplification and, 352
tuberculosis pathogenesis and, 266
putPA gene
rhizobacterial osmoadaptation and, 109
Pyrodinium bahamense
microalgal metabolites and, 455
Pyrrolnitrin
halogenated metabolites and, 387
Pyrrophyta
microalgal metabolites and, 434, 445–46

Q

Q-beta replicase (QBR)
nucleic acid amplification and, 353
Quaternary ammonium compounds
enteroviruses and, 9
Quiescent cells
bacterial cell size and, 329–30
Quinate
β-ketoadipate pathway and, 578
quiX gene
β-ketoadipate pathway and, 577
Quorum sensing
LuxR-LuxI type regulation and, 727–46

R

Random amplification of polymorphic RNA (RAPD)
evolutionary genetics and, 409–22, 425
Random mating
evolutionary genetics and, 415
Rapid plasma reagin
nucleic acid amplification and, 352
Rash
live attenuated varicella vaccine and, 81
rcs genes
LuxR-LuxI type regulation and, 743
Reactivation
live attenuated varicella vaccine and, 60, 68
recA genes
mycoplasmal molecular biology and, 38
Receptors
autoinducer, 738–40
oral bacteria adhesion mechanisms and, 519–20, 530–33
poliovirus, 14
T-cell, 825
Recombinant enzymes
genetically engineered synthesis and, 467
Recombination
evolutionary genetics and, 407–8, 411, 416, 425
Regulation
β-ketoadipate pathway and, 579–81
pectinolysis regulation in *E. chrysanthemi* and, 214–50
Regulatory cascades
LuxR-LuxI type regulation and, 742–43
Regulatory mechanism compensation
E. coli and, 668–69
Repartition
evolutionary genetics and, 421
Repetitive elements
mycoplasmas and, 31–32
Resistance genes
heavy metal resistances and, 778
Respiration
cobalamin synthesis and use, 138, 141
Respiratory diseases
nucleic acid amplification and, 354–55
Restriction fragment length polymorphism (RFLP)
evolutionary genetics and, 410–11, 422, 425
nucleic acid amplification and, 363–64
Restriction systems
mycoplasmas and, 43–44
Retortamonadida
G. lamblia and, 683
Reversible mutations
bacterial cell size and, 325–26
Reversion
evolutionary genetics and, 421, 426
spontaneous mutators and, 626
rfb genes
capsular polysaccharide production and, 297
Rhabdomyosarcoma (RD) cells
enteroviruses and, 10–11
Rhicadhesin
rhizobacterial osmoadaptation and, 125–26
Rhizobacteria
osmoadaptation by *Azospirillum*-associative symbiosis, 126
choline-derived glycine betaine as compatible solute, 117–18
compatible solute and osmoprotectant utilization by selected rhizobacteria, 111–18
compatible solute and osmoprotectant use by enteric bacteria, 108–10
compatible solute synthesis, 112–14
ectoine, 114, 116–17
future research, 127–29
glucosylglycerol, 114
glutamate synthesis, 112
glycine betaine, 114–15
hypoosmotic adaptation, 118–22
introduction, 102–3
NAGGN, 113
osmoadaptive responses of

free-living rhizobacteria, 107–22
osmoprotectant uptake, 114–17
osmotic stress effects on plant-microbe interactions, 122–27
periplasmic glucans, 118–22
potassium uptake, 112
proline, 112–13
proline betaine, 115–16
Pseudomonas-plant interactions, 126–27
Rhizobium-legume symbiosis, 123–26
rhizosphere structure and osmolality, 104–7
trehalose, 113, 116
Rhizobiaceae
rhizobacterial osmoadaptation and, 121
Rhizobium fredii
rhizobacterial osmoadaptation and, 113–14
Rhizobium leguminarosum
evolutionary genetics and, 417
β-ketoadipate pathway and, 568, 581
LuxR-LuxI type regulation and, 733, 742, 746
rhizobacterial osmoadaptation and, 113, 116, 120, 123
Rhizobium meliloti
capsular polysaccharide production and, 290, 300
evolutionary genetics and, 417–18
rhizobacterial osmoadaptation and, 103, 111–18, 120–25
Rhizobium spp.
β-ketoadipate pathway and, 558, 575–76
rhizobacterial osmoadaptation and, 101–2, 108, 111–12, 119, 123–26
Vibrio fischeri-Euprymna scolopes symbiosis and, 604
Rhizobium trifolii
β-ketoadipate pathway and, 562
Rhizoplane
rhizobacterial osmoadaptation and, 104
rhl genes
LuxR-LuxI type regulation and, 741, 743
Rhodococcus erythropolis
β-ketoadipate pathway and, 553, 563, 565, 575, 577
Rhodococcus spp.
β-ketoadipate pathway and, 556
Rhodomelaceae
microalgal metabolites and, 443
Rhodomicrobium vanneilii
bacterial cell size and, 328
Rhodophyta
microalgal metabolites and, 434
Rhodopseudomonas viridis
F_0F_1-ATPases and, 798
Rhodotorula spp.
β-ketoadipate pathway and, 558
Ribbons
G. lamblia and, 685
Ribonucleotide reductases
cobalamin synthesis and use, 147
Ribosomal RNA (rRNA)
cat-scratch disease and, 715
E. coli and, 645–70
G. lamblia and, 682–83
Rice blast
M. grisea and, 491
Rickettsia conorii
cat-scratch disease and, 714
Rickettsia rickettsii
cat-scratch disease and, 714
Rickettsia tsutsugamushi
cat-scratch disease and, 714
Rifampin
nucleic acid amplification and, 362
Rifampicin
spontaneous mutators and, 639
Ring carbons
cobalamin synthesis and use, 140, 152
RNA polymerases
LuxR-LuxI type regulation and, 741, 746
rRNA transcription in *E. coli* and, 645
RNA world
cobalamin synthesis and use, 140
Rochalimaea henselae
cat-scratch disease and, 707, 715–19
Rochalimaea quintana
cat-scratch disease and, 715–16
Rochalimaea spp.
cat-scratch disease and, 715–19
rol gene
capsular polysaccharide production and, 291
Rough endoplasmic reticulum (RER)
G. lamblia and, 683
rpoS gene
LuxR-LuxI type regulation and, 745
rhizobacterial osmoadaptation and, 128
RSY1 gene
M. grisea and, 501–2
Ruminococcus albus
polysaccharide hydrolysis and, 196
Ruminococcus flavefaciens
polysaccharide hydrolysis and, 196

S

Saccharomyces cerevisiae
G. lamblia and, 684
polysaccharide hydrolysis and, 195
Saccharomyces spp.
G. lamblia and, 683
S-adenosyl methionine (SAM)
genetically engineered synthesis and, 471
Salivary proteins
oral bacteria adhesion mechanisms and, 519–20
Salmonella enterica
capsular polysaccharide production and, 292
Salmonella spp.
cobalamin synthesis and use, 138, 144, 146, 173
evolutionary genetics and, 418
Salmonella typhi
capsular polysaccharide production and, 288, 290, 296
Salmonella typhimurium
bacterial cell size and, 325
capsular polysaccharide production and, 297
cobalamin synthesis and use, 138–39, 141, 145, 148–67, 171–73
rhizobacterial osmoadaptation and, 103, 108–10, 114, 118, 128
spontaneous mutators and, 629
Saprophytes
bacterial cell size and, 339, 344
tuberculosis pathogenesis and, 259, 272–74
Saxitonin
microalgal metabolites and, 435–36
Scanning electron microscopy (SEM)
G. lamblia and, 685
Scavenging

bacterial cell size and, 331
Scytonema spp.
microalgal metabolites and, 440, 443
Seasonality
poliovirus and, 5
Secondary infections
tuberculosis pathogenesis and, 260
Secretory pathways
G. lamblia and, 679
Segregation
evolutionary genetics and, 407–8, 424, 426
Selectable markers
mycoplasmas and, 40–41
Selection
evolutionary genetics and, 418
β-ketoadipate pathway and, 582–83
Self-identity
biology of, 553–83
Selfing
evolutionary genetics and, 416
Self-sustaining sequence replication (3SR)
nucleic acid amplification and, 353
serA gene
capsular polysaccharide production and, 293, 296, 307
Serology
limitations of, 352
poliovirus and, 4
Serratia liquefaciens
polysaccharide hydrolysis and, 194
Serratia marcescens
halogenated metabolites and, 390
LuxR-LuxI type regulation and, 733
polysaccharide hydrolysis and, 194
Serratia spp.
cobalamin synthesis and use, 172
Sewage
poliovirus and, 3
Sexual species
evolutionary genetics and, 401, 404, 406–7, 414, 416–18, 423
Shellfish poisoning
microalgal metabolites and, 431, 458
Shell nature
bacterial cell size and, 341–42
Shikimate
β-ketoadipate pathway and, 578
Shine-Delgarno sequence
mycoplasmal molecular biology and, 34
Shingles
live attenuated varicella vaccine and, 60, 64, 77–78
'Shut down' cell
bacterial cell size and, 328–29, 344
Sialyl T-antigen synthesis
genetically engineered synthesis and, 474, 476
Signal amplification
nucleic acid amplification and, 353
Silver
heavy metal resistances and, 781
Siroheme
cobalamin synthesis and use, 138, 140–41
Site-specific DNA inversion
mycoplasmas and, 39–40
Site-specific recombination
mycoplasmas and, 38–40
Skin-test reactivity
tuberculosis pathogenesis and, 259, 273–74
Slippage
bacterial cell size and, 326
Slipped-strand mispairing
mycoplasmal molecular biology and, 48
sod genes
spontaneous mutators and, 629, 634–35
Sodium chloride
rhizobacterial osmoadaptation and, 104, 106–7, 116–17, 125
Sodium dodecyl sulfate (SDS)
enteroviruses and, 12
Soil microbes
heavy metal resistances and, 754
Soil water
rhizobacterial osmoadaptation and, 101, 104–5
Sorting functions
G. lamblia and, 679
soxR locus
spontaneous mutators and, 629
Space
evolutionary genetics and, 401, 410
Specialist markers
evolutionary genetics and, 422
Specific host immunity
capsular polysaccharide production and, 287, 289
Specificity
Vibrio fischeri-Euprymna scolopes symbiosis and, 591, 598–601
Spiking
nucleic acid amplification and, 352
Spiroplasma citri
mycoplasmal molecular biology and, 29, 32–33, 38–39, 41, 43–44
Spiroplasma spp.
mycoplasmal molecular biology and, 28, 32, 36, 44
Spontaneous mutators
detection of mutators, 626–27
historical perspective, 626–27
introduction, 626
mutagenetic pathways
additional mutators, 633–35
mutator tRNAs, 632–33
mutators and cancer, 638–39
mutators and origin of spontaneous mutations, 634, 636–37
transient mutations, 637–38
repair and error avoidance systems revealed by mutators
GO system for oxidative repair, 630–31
mismatch repair, 628–29
oxidative damage prevention, 629
proofreading, 628
Spore tip mucilage
M. grisea and, 495
Staphylococcus aureus
bacterial cell size and, 323
capsular polysaccharide production and, 304, 306
evolutionary genetics and, 420
heavy metal resistances and, 767, 772, 777
live attenuated varicella vaccine and, 69
LuxR-LuxI type regulation and, 745
Staphylococcus xylosus
heavy metal resistances and, 767
Starch
polysaccharide hydrolysis and, 183–84, 193
Starvation conditions
bacterial cell size and, 333–34
Stationary phase induction
pectinolysis regulation in

E. chrysanthemi and, 229–30
Statistical error
type II
evolutionary genetics and, 419–20
Sterols
microalgal metabolites and, 433, 435
Stock
evolutionary genetics and, 426
Strain typing
evolutionary genetics and, 403–5, 412–13
Strand displacement amplification (SDA)
nucleic acid amplification and, 353
Streptococcus group A
nucleic acid amplification and, 351, 355
Streptococcus group B
capsular polysaccharide production and, 304
Streptococcus pneumoniae
capsular polysaccharide production and, 304–8
mycoplasmal molecular biology and, 37
nucleic acid amplification and, 355
Streptococcus pyogenes
live attenuated varicella vaccine and, 69
nucleic acid amplification and, 355
Streptococcus spp.
oral bacteria adhesion mechanisms and, 520–33
Streptomyces antibioticus
halogenated metabolites and, 379
Streptomyces aureofaciens
halogenated metabolites and, 378, 384–85, 390, 393
Streptomyces calvus
halogenated metabolites and, 380
Streptomyces cattleya
halogenated metabolites and, 383, 387
Streptomyces cinnamonensis
cobalamin synthesis and use, 148
microalgal metabolites and, 451
Streptomyces halstedii
polysaccharide hydrolysis and, 199
Streptomyces lividans
F_0F_1-ATPases and, 806
halogenated metabolites and, 390
heavy metal resistances and, 773
polysaccharide hydrolysis and, 191, 194, 199–200
Streptomyces mediocidicus spp.
microalgal metabolites and, 445
Streptomyces olivaceoviridis
polysaccharide hydrolysis and, 191–92, 194
Streptomyces olivaceus
cobalamin synthesis and use, 156
Streptomyces phaeochromogenes
halogenated metabolites and, 389
Streptomyces plicatus
polysaccharide hydrolysis and, 194
Streptomyces reticuli
polysaccharide hydrolysis and, 199
Streptomyces rugosporus
halogenated metabolites and, 378
Streptomyces spp.
halogenated metabolites and, 383, 389
heavy metal resistances and, 773, 776
β-ketoadipate pathway and, 581
LuxR-LuxI type regulation and, 728, 745
microalgal metabolites and, 439, 443, 445, 447, 458
nucleic acid amplification and, 362
polysaccharide hydrolysis and, 194, 200
Streptomyces thermoviolaceus
polysaccharide hydrolysis and, 194
Streptomyces venezuelae
halogenated metabolites and, 377–78, 386–87, 391–92
Structural variations
genetically engineered synthesis and, 467
Subgingival occupants
oral bacteria adhesion mechanisms and, 517–19
Substrate-activated death
bacterial cell size and, 334
Sulfite
cobalamin synthesis and use, 140
Supraoperonic clustering
β-ketoadipate pathway and, 575, 577–79
Surface proteins
G. lamblia and, 679
Surface-to-volume question
bacterial cell size and, 339–40
Symbiodinium spp.
microalgal metabolites and, 441, 444, 459
Symbiosis
rhizobacterial osmoadaptation and, 123–26
Vibrio fischeri-Euprymna scolopes, 591–618
Sympatry
evolutionary genetics and, 413, 426
Sym plasmid pRLJ1
LuxR-LuxI type regulation and, 742
Synapomorphy
evolutionary genetics and, 409, 413, 426
Synechococcus spp.
heavy metal resistances and, 779–80
Synechocystis spp.
heavy metal resistances and, 755
Synthetic approach
evolutionary genetics and, 402
Systemic disease
nucleic acid amplification and, 356–57

T

Target amplification
nucleic acid amplification and, 353
Taxonomy
capsular polysaccharide production and, 287, 298
evolutionary genetics and, 401–2, 404–5, 413–14, 418, 422, 426
microalgal metabolites and, 431, 433, 435–46
T-cells
HIV mechanisms of disease and, 825
tuberculosis pathogenesis and, 263–64, 273
Teeth
oral bacteria adhesion mechanisms and, 513
Tellurite
heavy metal resistances and, 781–82
Temperature
bacterial cell size and, 341
pectinolysis regulation in

E. chrysanthemi and, 214, 232
Termination
premature
rRNA transcription in *E. coli* and, 645
tetM gene
mycoplasmal molecular biology and, 40–44
Tetrahydrofolate
cobalamin synthesis and use, 145
Tetrathionate
cobalamin synthesis and use, 138
T gene
capsular polysaccharide production and, 295, 298
Thallous resistance systems
heavy metal resistances and, 781
Theonella swinhoei
microalgal metabolites and, 459
Thermomonospora fusca
polysaccharide hydrolysis and, 200–1, 203
Thermoregulation
pectinolysis regulation in *E. chrysanthemi* and, 232
Thermus thermophilus
F_0F_1-ATPases and, 793
Thiobacillus spp.
heavy metal resistances and, 770–71
Thyroxine
halogenated metabolites and, 377
Time
bacterial cell size and, 341
evolutionary genetics and, 401, 410
oral bacteria adhesion mechanisms and, 517–19
Tin
heavy metal resistances and, 755
Ti plasmid conjugal transfer
LuxR-LuxI type regulation and, 728, 730, 741–42
TN*916*
mycoplasmas and, 42–43
tnpA gene
capsular polysaccharide production and, 305
Tolypothrix conglutinata
microalgal metabolites and, 440
TonB protein
cobalamin synthesis and use, 159, 161–62
Topology
F_0F_1-ATPases and, 795–801
Toxoplasma gondii
evolutionary genetics and, 406, 414–15
nucleic acid amplification and, 356
Trachea
tuberculosis pathogenesis and, 270–71, 274
tra genes
LuxR-LuxI type regulation and, 740–42
trans-acting contributors
rRNA transcription in *E. coli* and, 649–62
Transcription
E. coli and, 645–70
mycoplasmas and, 33
pectinolysis regulation in *E. chrysanthemi* and, 214
Transcriptional mediated amplification (TMA)
nucleic acid amplification and, 353
Transcriptional regulation
LuxR-LuxI and, 727–46
Transduction
Vibrio fischeri-Euprymna scolopes symbiosis and, 610
Transfer RNA (tRNA)
bacterial cell size and, 338
spontaneous mutators and, 632–33
Transformation
mycoplasmas and, 41–42
Transient mutations
spontaneous mutators and, 637–38
Translation
mycoplasmas and, 33–34
Transport
G. lamblia and, 679, 682–84, 694–700
β-ketoadipate pathway and, 569–73
Transposable elements
mycoplasmas and, 38–39
treBC operon
rhizobacterial osmoadaptation and, 109–10
Trehalose
rhizobacterial osmoadaptation and, 108, 110–11, 113, 116
Treponema denticola
oral bacteria adhesion mechanisms and, 541
Treponema pallidum
nucleic acid amplification and, 359–61
Treponema spp.
oral bacteria adhesion mechanisms and, 539–40
Tricarboxylic acid cycle intermediates
β-ketoadipate pathway and, 553
Trichoderma reesei
polysaccharide hydrolysis and, 191, 195, 201
Trichosporon cutaneum
β-ketoadipate pathway and, 558, 565–66
Trigonelline
rhizobacterial osmoadaptation and, 124
trk genes
rhizobacterial osmoadaptation and, 109
Tropheryma whippelii
nucleic acid amplification and, 351–52, 362
Trophozoite
G. lamblia and, 679–82, 684–86
trp gene
capsular polysaccharide production and, 292
Trypanosoma brucei
evolutionary genetics and, 411, 414–15, 418, 420
Trypanosoma cruzi
evolutionary genetics and, 403, 406, 409, 412–15, 418
Trypanosoma spp.
evolutionary genetics and, 408
TSA 417
G. lamblia and, 696–98, 700
Tuberculosis
antigens involved in protection and immunopathology
environmental mycobacteria and regulation of T cell response to pathogens, 273
immunotherapy, 274–75
loss of skin-test positivity to common epitopes during active disease, 273–74
current world situation, 260
factors that deregulate type 1 response
adrenal function, 278
glucocorticoids, 277
peripheral regulation of cortisol-mediated effects, 277–78
vitamin D_3 metabolism in tuberculous lesions, 275–77
mechanism of protective immunity
antibody role, 265

avoidance of macrophage-mediated killing, 264–65
CD1 restricted recognition of mycobacterial lipids and glycolipids, 263–64
MHC class 1-restricted cells, 262–63
nitric oxide and antimycobacterial pathways of macrophages, 264
pattern of response associated with immunity in humans, 265–66
T cell subsets of unknown protective role, 263–64
TNFα as protective cytokine, 264
type I response, 262
mechanisms of immunopathology
cytokine-sensitivity of mycobacterial lesions, 267
effect of priming mixed Th1+Th2 or Th0 response pattern before infection, 269 271, 274
Koch phenomenon, 266–67, 271–72
mixed patterns of cytokine expression and tissue damage, 268–69
mixed patterns of cytokine expression in tuberculosis, 267–68
M. tuberculosis toxicity, 266
TNFα-mediated toxicity during murine tuberculosis, 269–70
problem of six-month treatment regimen, 261
Tubulins
G. lamblia and, 686
tuf gene
mycoplasmal molecular biology and, 34
Tumor necrosis factor α (TNF-α)
tuberculosis pathogenesis and, 264, 269–70, 274
Turgor pressure
M. grisea and, 491, 503–6

U

Udotea flabellum
microalgal metabolites and, 446
Udotea spp.
microalgal metabolites and, 448
Ulcerative disease
nucleic acid amplification and, 360–61
Ultracentrifugation
poliovirus and, 2–3
Ultramicrobacteria
bacterial cell size and, 340
Ultramicroorganisms
bacterial cell size and, 341
Ultrastructure
G. lamblia and, 679, 684–87
unc operon
F_0F_1-ATPases and, 793
ung genes
spontaneous mutators and, 633, 635
United Kingdom
tuberculosis pathogenesis and, 260
United States
live attenuated varicella vaccine and, 79–85, 88
Unstirred layer
bacterial cell size and, 337
Unweighted pair-group method with arithmetic averages (UPGMA)
evolutionary genetics and, 417, 426
UP element
rRNA transcription in *E. coli* and, 651–53
Upper hyperbolic curve
bacterial cell size and, 332
Ureaplasma spp.
mycoplasmal molecular biology and, 28
Ureaplasma urealyticum
mycoplasmal molecular biology and, 29–30, 42–43, 48
Urethritis
nucleic acid amplification and, 360
UroIII
cobalamin synthesis and use, 139–41, 148, 153
uvr genes
mycoplasmal molecular biology and, 37
spontaneous mutators and, 628–29, 635

V

Vaccination
poliovirus and, 6–8
Vaccine design
evolutionary genetics and, 405–6
varicella, 59–90
VAI-1
LuxR-LuxI type regulation and, 727–28, 730–32, 739–40, 742
Vibrio fischeri-Euprymna scolopes symbiosis and, 596–97, 602, 617
VAI-2
LuxR-LuxI type regulation and, 745
Vibrio fischeri-Euprymna scolopes symbiosis and, 596–97, 617
Vanadium-containing nonheme haloperoxidases
halogenated metabolites and, 389
Variant surface proteins (VSPs)
G. lamblia and, 694–97
Varicella (VZV) vaccine, live attenuated
active immunization
early studies in Japan, 79
Japanese studies, 78–79
Oka strain development, 78
antiviral therapy
herpes zoster, 77–78
varicella, 76–77
clinical manifestations
herpes zoster, 71–73
varicella, 69–71
epidemiology, 63–64
herpes zoster, 64
immunization of healthy children
dosage impact, 86
persistence of immunity in healthy children, 87
post-exposure prophylaxis, 87
safety, 85
vaccine efficacy, 85–86
introduction, 60
naturally acquired immunity to VZV
cell-mediated immunity, 74–75
humoral immunity, 73
passive antibody prophylaxis, 75
pathogenesis
latency, 67–68
primary infection, 64–67
reactivation, 68
preventing zoster in those with prior wild-type infection, 88
primary infection, 67
recommendations for use of varicella vaccine in U.S.
cost-benefit studies, 89

potential for spread of vaccine virus, 88–89
simultaneous administration with other vaccines, 87
United States and Canadian collaborative studies
efficacy data, 82
immunization and zoster, 82–83
immunocompromised children, 83–84
immunogenicity and correlates of immunity, 81–82
leukemic vaccines, 79–80
persistence of immunity, 82
rash, 81
safety, 80–81
vaccine type VZV, 81, 83
varicella-susceptible adults, 84–85
virus overview, 61–63
Veillonella spp.
oral bacteria adhesion mechanisms and, 540
Very short patch (VSP) repair pathway
spontaneous mutators and, 633–34
Viable-but-not-culturable (VNBC) bacteria
bacterial cell size and, 331–33, 344
Vibrio fischeri
LuxR-LuxI type regulation and, 727–32, 739–40, 743–46
Vibrio fischeri-Euprymna scolopes symbiosis
bioluminescence in *V. fischeri*, 596–97
colonization of nascent *E. scolopes* light organ
bacterial responses, 601–4
competition between *V. fischeri* strains, 608–9
experimental colonization assay, 597–98
host development program, 604–7
host responses, 604–7
maintenance of association, 608–9
modulation of light organ luminescence, 607–8
species specificity of association, 598–601
E. scolopes light organ, 594–96
flagellation, 602–4
genetic determinants of symbiotic competency in *V. fischeri*, amino acid auxotrophy, 616
genetic determinants of symbiotic competency in *V. fischeri*
autoinducers, 616–17
cAMP utilization, 616
gene transfer, 610
iron sequestration, 615
location of symbiotic determinants, 611–12
luminescence, 614–15
molecular genetic approaches and tools for studies, 609–12
motility, 612–14
mutagenesis, 611
using *V. fischeri* mutants to characterize light organ crypt environment, 612–17
introduction, 592–97
luminescence, 601–2
symbiotic partners, 593–94
Vibrio harveyi
LuxR-LuxI type regulation and, 729, 731–32, 735, 739, 744
Virulence
evolutionary genetics and, 405, 407
Virologic events
bacterial cell size and, 338
HIV mechanisms of disease and, 825, 831–35, 840, 844–45, 848–49
Virus escape mechanisms
HIV mechanisms of disease and, 825
Vitamin B_{12}, see Cobalamin
Vitamin D_3
tuberculosis pathogenesis and, 275–77
vlp genes
mycoplasmal molecular biology and, 46–48
vsa genes
mycoplasmal molecular biology and, 39–40, 46–48
vsp genes
mycoplasmal molecular biology and, 48

W

Wagner method
evolutionary genetics and, 410
WAI
nucleic acid amplification and, 357
Waste products
bacterial cell size and, 317
Whipple's-associated bacillus
nucleic acid amplification and, 351, 362
WI-38 cells
enteroviruses and, 14
Wild-type cells
β-ketoadipate pathway and, 572
live attenuated varicella vaccine and, 88
spontaneous mutators and, 625
Wilson's disease
heavy metal resistances and, 758–61
World Health Organization (WHO)
enteroviruses and, 11
tuberculosis pathogenesis and, 260

X

Xanthobacter autrophicus
halogenated metabolites and, 393
Xanthomonas campestris
capsular polysaccharide production and, 304
Xanthomonas spp.
rhizobacterial osmoadaptation and, 102
Xanthophyta
microalgal metabolites and, 434
xth gene
spontaneous mutators and, 634

Y

Yeasts
evolutionary genetics and, 416
yen genes
LuxR-LuxI type regulation and, 741
Yersinia enterocolitica
evolutionary genetics and, 417
LuxR-LuxI type regulation and, 733

Z

Zymodeme
evolutionary genetics and, 419, 426